

162249

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From: Swope, Sheridan
Sent: Thursday, August 11, 2005 12:01 PM
To: STIC-Biotech/ChemLib
Subject: 10/726,967

For 10/726,967, pls search:

SID 84 against the NT and AA data bases.

Thanks

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

CRFE

Paula Shoppard

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2005, 08:05:28 ; Search time 132 Seconds
(without alignments)
1679.775 Million cell updates/sec

Title: US-10-726-967a-84

Perfect score: 2288
Sequence: 1 TQHGIRLPRLRSGLGAPLGL.....FVTLMDPCGNIPQTBEST 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2267	99.1	501	BAE1_HUMAN	P56817 homo sapien
2	2261	98.8	501	Q81YC8	P56819 r beta-secr
3	2218	96.9	501	BAE1_RAT	P56818 mus musculu
4	2216	96.9	501	BAE1_MOUSE	08C7R1 mus musculu
5	2215	96.8	501	08C7R1	08b9Y4 mus musculu
6	2211	96.6	501	08B9Y4	09ULB1 homo sapien
7	2204	96.3	532	09ULS1	08C4F4 mus musculu
8	2023	88.4	467	08C4F4	06NZT7 brachydanto
9	1794	78.4	505	06NZT7	069ZG6 mus musculu
10	1711	74.8	373	069ZG6	09J118 mus musculu
11	1163	50.8	267	09CUT5	09J5D0 homo sapien
12	1136	49.7	518	BAE2_HUMAN	09H2V8 homo sapien
13	1121	49.0	439	09H2V8	08C5E9 mus musculu
14	1120	49.0	514	08C5E9	06IET5 rattus norv
15	1120	49.0	514	09J118	08C7R3 mus musculu
16	1117	48.8	514	06IET5	06b2D0 xenopus lae
17	1115	48.7	514	08C7R3	07C0Y2 xenopus lae
18	1070	46.8	499	06B2D0	08N2D4 homo sapien
19	1061	46.4	500	07T0Y2	09N2L1 homo sapien
20	1038	45.4	423	08N2D4	09N2L2 homo sapien
21	971.5	42.5	396	09N2L1	09P0D2 homo sapien
22	937	41.0	468	09N2L2	09P0D2 homo sapien
23	712.5	31.1	213	09P0D2	09P0D2 homo sapien
24	566.5	23.2	255	09P0D2	09P0D2 homo sapien
25	530	23.2	127	07G6P0	08WQY9 aphrocallis
26	359.5	15.7	244	08WQY9	08N6S8 xenopus lae
27	345	15.1	76	08N6S8	06P7F8 xenopus lae
28	336.5	14.7	392	06P7F8	09VKK6 drosophila
29	332.5	14.5	391	09VKK6	09VKK6 drosophila
30	332	14.5	354	09GTX7	09GTX7 boophilus m
31	327	14.3	324	PEP1_GADMO	P56272 gadus morhua

ALIGNMENTS

32	314.5	13.7	390	1	CATD_BOVIN	P80209 bos taurus
33	314	13.7	397	1	CTE2_XENLA	Q805F2 xenopus lae
34	312.5	13.7	386	2	09BGU5	Q805F2 xenopus lae
35	311	13.6	387	1	PEP1_RABIT	P28712 oryctolagus
36	309	13.5	384	2	Q9DEC2	Q9dec2 xenopus lae
37	308	13.5	385	2	Q9DEC4	Q9dec4 rana catesb
38	308	13.5	397	1	CTE1_XENLA	Q805F3 xenopus lae
39	307.5	13.4	401	2	06INM6	06inm6 xenopus lae
40	307	13.4	386	2	06HA02	06ha02 brachydanto
41	306	13.4	412	2	06GRT7	06gtr7 rhinoloophus
42	305	13.3	386	2	09GMY7	09gmy7 sorex ungu
43	305	13.3	387	2	09GMY8	09gmy8 drosophila
44	304.5	13.3	372	2	09VTK3	09vtk3 drosophila
45	304.5	13.3	383	2	Q9DEC3	Q9dec3 xenopus lae

RESULT 1

BAE1_HUMAN	STANDARD	PRT	501 AA.
AC	P56817; Q9BYB9; Q9BYC0; Q9BYC1; Q9UT5;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Beta-secretase 1 precursor (EC 3.4.23.46) (Beta-site APP cleaving enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)		
DE	(Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic protease 2) (Memapsin-2).		
GN	Name=BACE1; Synonyms=BACE;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM A).		
RC	TISSUE=Brain;		
RX	MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;		
RA	Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,		
RA	Denis P., Teplow D.B., Ross S., Amarante P., Loebner J., Luo Y.,		
RA	Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,		
RA	Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,		
RA	Treanor J., Rogers G., Citron M.,		
RT	"Beta-secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane aspartic protease BACE."		
RL	Science 286:735-741(1999).		
RN	[2]		
RP	SEQUENCE FROM N.A. (ISOFORM A), SEQUENCE OF 46-68, AND CHARACTERIZATION.		
RC	TISSUE=Brain;		
RX	MEDLINE=20057171; PubMed=10591214; DOI=10.1038/990114;		
RA	Sinha S., Anderson J.P., Barbour R., Basl G.S., Caccavelli R.,		
RA	Davis D., Doan M., Dorey H.F., Frigon N., Hong J., Jacobson-Croak K.,		
RA	Jewett N., Keim P., Knops J., Lieberburg I., Power M., Tan H.,		
RA	Tateo G., Tung J., Schenk D., Seubert P., Suematsu S.M., Wang S.,		
RA	Walker D., Zhao J., McConlogue L., Varghese J.,		
RT	"Purification and cloning of amyloid precursor protein beta-secretase from human brain."		
RL	Nature 402:537-540(1999).		
RN	[3]		
RP	SEQUENCE FROM N.A. (ISOFORM A)		
RX	MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;		
RA	Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,		
RA	Brashear J.R., Strattan N.C., Mathews W.R., Buhl A.E., Carter D.B.,		
RA	Tomasek J.A., Parodi L.A., Heinkeon R.L., Gurney M.E.,		
RT	"Membrane-anchored aspartyl protease with Alzheimer's disease beta-secretase activity."		
RL	Nature 402:533-537(1999).		
RN	[4]		
RP	SEQUENCE FROM N.A. (ISOFORM A).		
RX	MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811;		
RA	Hussein I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,		

FT STRAND 211 215
FT HELIX 224 229

Query Match 99.1%; Score 2267; DB 1; Length 501;
Best Local Similarity 99.1%; Pred. No. 5.3e-174;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TONGIRLPLRSGLGAPLGLEINLETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
DB 22 TONGIRLPLRSGLGAPLGRLPRETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 81
QY 61 GSPPTNLILVDTGSSNFAVGAAPHPFLHRYQROLSTYRDLRGVVPVPTQGMBGL 120
DB 82 GSPPTNLILVDTGSSNFAVGAAPHPFLHRYQROLSTYRDLRGVVPVPTQGMBGL 141
QY 121 GTDLVSIHGPVNTVRANIAAITEEDKFFINGSMNEGILGLAYAEIARPDLSLEFPDSL 180
DB 142 GTDLVSIHGPVNTVRANIAAITEEDKFFINGSMNEGILGLAYAEIARPDLSLEFPDSL 201
QY 181 VKQTHVPLFSLQLCGAGFPLNOSFVLASVGGSMIIGIDHSLYTGSLMYTPIRREWYE 240
DB 202 VKQTHVPLFSLQLCGAGFPLNOSFVLASVGGSMIIGIDHSLYTGSLMYTPIRREWYE 261
QY 241 VIVAVEINGODLKMDCCKEYNDKSIIVDSGTTNLRPKKVFBAAVKSIKAASTKFPDG 300
DB 262 VIVAVEINGODLKMDCCKEYNDKSIIVDSGTTNLRPKKVFBAAVKSIKAASTKFPDG 321
QY 301 FVLGSQLVCMQAGTTPMNIIFPVISLYLMGEVTVNOSFRITILPQOYLRPVEDVATSDDCY 360
DB 322 FVLGSQLVCMQAGTTPMNIIFPVISLYLMGEVTVNOSFRITILPQOYLRPVEDVATSDDCY 381
QY 361 KFAISOSTGTGAVINMEGFVVDPRARKRIGFAVSAHVDEFRTAAVEGPFYTLDM 420
DB 382 KFAISOSTGTGAVINMEGFVVDPRARKRIGFAVSAHVDEFRTAAVEGPFYTLDM 441
QY 421 DCGYNIPOTDEST 433
DB 442 DCGYNIPOTDEST 454
```

RESULT 2

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08IYC8 PRELIMINARY; PRT; 501 AA.
AC 08IYC8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Beta-site App-cleaving enzyme 1, isoform A preproprotein.
GN Name=BACE1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,
RA Altshuler R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Mullaney S.J.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
```

RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN (2)
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC -1 SIMILARITY: Belongs to peptidase family A1.

DR EMBL: BC036084; AAH36084.1; -.

DR HSSP: P56817; 1FKN.

DR GO: GO:0005794; C:Golgi apparatus; ISS.

DR GO: GO:0016021; C:Integral to membrane; ISS.

DR GO: GO:0004190; F:aspartic-type endopeptidase activity; ISS.

DR GO: GO:0050435; P:beta-amyloid metabolism; ISS.

DR GO: GO:0006509; P:membrane protein ectodomain proteolysis; ISS.

DR InterPro: IPR001461; Peptidase A1.

DR InterPro: IPR009119; Pept_A1_BACE.

DR InterPro: IPR009120; Pept_A1_BACE1.

DR InterPro: IPR009007; Pept_Aspartic.

DR InterPro: IPR001969; Pept_Asp_AS.

DR PRINTS: PR01816; BACE1.

DR PRINTS: PR00792; PERSIN.

DR PROSITE: PS00141; ASP_PROTEASE; 1.

KW Aspartyl1 protease; Hydroxylase; Protease;

SEQUENCE 501 AA; 55823 MW; 768595CF5517EFB7 CRC64;

Query Match 98.8%; Score 2261; DB 2; Length 501;

Best Local Similarity 98.8%; Pred. No. 1.6e-173; Indels 0; Gaps 0;
Matches 428; Conservative 1; Mismatches 4;

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QY 1 TONGIRLPLRSGLGAPLGLEINLETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
DB 22 TONGIRLPLRSGLGAPLGRLPRETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 81
QY 61 GSPPTNLILVDTGSSNFAVGAAPHPFLHRYQROLSTYRDLRGVVPVPTQGMBGL 120
DB 82 GSPPTNLILVDTGSSNFAVGAAPHPFLHRYQROLSTYRDLRGVVPVPTQGMBGL 141
QY 121 GTDLVSIHGPVNTVRANIAAITEEDKFFINGSMNEGILGLAYAEIARPDLSLEFPDSL 180
DB 142 GTDLVSIHGPVNTVRANIAAITEEDKFFINGSMNEGILGLAYAEIARPDLSLEFPDSL 201
QY 181 VKQTHVPLFSLQLCGAGFPLNOSFVLASVGGSMIIGIDHSLYTGSLMYTPIRREWYE 240
DB 202 VKQTHVPLFSLQLCGAGFPLNOSFVLASVGGSMIIGIDHSLYTGSLMYTPIRREWYE 261
QY 241 VIVAVEINGODLKMDCCKEYNDKSIIVDSGTTNLRPKKVFBAAVKSIKAASTKFPDG 300
DB 262 VIVAVEINGODLKMDCCKEYNDKSIIVDSGTTNLRPKKVFBAAVKSIKAASTKFPDG 321
QY 301 FVLGSQLVCMQAGTTPMNIIFPVISLYLMGEVTVNOSFRITILPQOYLRPVEDVATSDDCY 360
DB 322 FVLGSQLVCMQAGTTPMNIIFPVISLYLMGEVTVNOSFRITILPQOYLRPVEDVATSDDCY 381
QY 361 KFAISOSTGTGAVINMEGFVVDPRARKRIGFAVSAHVDEFRTAAVEGPFYTLDM 420
DB 382 KFAISOSTGTGAVINMEGFVVDPRARKRIGFAVSAHVDEFRTAAVEGPFYTLDM 441
QY 421 DCGYNIPOTDEST 433
DB 442 DCGYNIPOTDEST 454
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RESULT 3

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BAE1 RAT STANDARD; PRT; 501 AA.
ID BAE1 RAT
AC P56819;
DT 30-MAY-2000 (rel. 39, Last sequence update)
```

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Beta-secretase 1 precursor (EC 3.4.23.46) (beta-site APP cleaving
 DE enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
 DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN Name=BACE1; Synonyms=BACE;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Rose S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 CC -1- FUNCTION: Responsible for the proteolytic processing of the
 CC amyloid precursor protein (APP). Cleaves at the amino terminus of
 CC the A-beta peptide sequence, between residues 671 and 672 of APP,
 CC leads to the generation and extracellular release of beta-cleaved
 CC fragment APP, and a corresponding cell-associated carboxy-terminal
 CC fragment which is later released by gamma-secretase (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Ala-Leu-Ileu-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the peptidase A1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF190727; AAF04144.1; -.
 DR HSSP; P56817; 1M4H.
 DR MEROPS; A01.004; -.
 DR RCD; 2191; BACE.
 DR InterPro; IPR009119; Pept_A1_BACE.
 DR InterPro; IPR009120; Pept_A1_BACE1.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR InterPro; IPR009007; Pept_AspArtic.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; Asp_1.
 DR PRINTS; PR01816; BACE1.
 DR PRINTS; PR01815; BACEFAMILY.
 DR PRINTS; PR00792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR KMW Aspartyl protease; Glycoprotein; Hydrolyase; Signal; Transmembrane;
 DR Zymogen.
 FT SIGNAL 1 21 Potential.
 FT PROPEP 22 45 Potential.
 FT CHAIN 46 501 Beta-secretase 1.
 FT DOMAIN 22 457 Extracellular (Potential).
 FT TRANSMEM 458 478 Potential.
 FT ACT_SITE 479 501 Cytoplasmic (Potential).
 FT ACT_SITE 289 93 By similarity.
 FT ACT_SITE 289 289 By similarity.
 FT DISULFID 216 420 By similarity.
 FT DISULFID 278 443 By similarity.
 FT DISULFID 330 380 By similarity.
 FT CARBOHYD 153 172 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 223 223 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 354 354 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 501 AA; 55806 MW; 24B45BCBBE87DE3 CRC64;
 Query Match 96.9%; Score 2218; DB 1; Length 501;
 Best Local Similarity 96.5%; Pred. No. 4.7e-170;
 Matches 418; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 QY 1 TGHGRLPLRSGLGAPILGLEINLETDEEPEPRRSGSFVEMVNLKSGSGGYVMTV 60
 DB 22 THGIRLPLRSGLAPPLGLRLPRTDDEPEPRRSGSFVEMVNLKSGSGGYVMTV 81
 QY 61 GSPPTNIIIVDTGSSNFAVGAAPHPPLHRYQRLSTTRDLRKGYVYPTGKMEGL 120
 DB 82 GSPPTNIIIVDTGSSNFAVGAAPHPPLHRYQRLSTTRDLRKGYVYPTGKMEGL 141
 QY 121 GTDLVSIHGNVTVYRANIAITSDKPFINGSMWEGILGLAVETARPDDSLPEPDSL 180
 DB 142 GTDLVSIHGNVTVYRANIAITSDKPFINGSMWEGILGLAVETARPDDSLPEPDSL 201
 QY 181 VKQTHVPMPLFSLQCGAGFPLNGSEVLAVSGSMITGIDHSLVYTGSLWYTPIRREMYE 240
 DB 202 VKQTHVPMPLFSLQCGAGFPLNGSEVLAVSGSMITGIDHSLVYTGSLWYTPIRREMYE 261
 QY 241 VTIYVEINQGLDKMDKEVYDKSYDSTTNLRPLPKYFEAAVKSIRKASTETKPPDG 300
 DB 262 VTIYVEINQGLDKMDKEVYDKSYDSTTNLRPLPKYFEAAVKSIRKASTETKPPDG 321
 QY 301 FWLGEQLVCMQAGTTPNNIFPVISLYLMGEVTVNQSFRTITLPQOYLRPYEDVATSDDDCY 360
 DB 322 FWLGEQLVCMQAGTTPNNIFPVISLYLMGEVTVNQSFRTITLPQOYLRPYEDVATSDDDCY 381
 QY 361 KEAISGSSSTGVGAVIMGEFYVFPDARKRIGFAVSACHVDEFTAAVEGPFVTLDE 420
 DB 382 KEAISGSSSTGVGAVIMGEFYVFPDARKRIGFAVSACHVDEFTAAVEGPFVTLDE 441
 QY 421 DCGYNIPQTDST 433
 DB 442 DCGYNIPQTDST 454
 RESULT 4
 BAE1 MOUSE STANDARD; PRT; 501 AA.
 AC P56818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Beta-secretase 1 precursor (EC 3.4.23.46) (beta-site APP cleaving
 DE enzyme 1) (Beta-site amyloid precursor protein cleaving enzyme 1)
 DE (Aspartyl protease 2) (Asp 2) (ASP2) (Membrane-associated aspartic
 DE protease 2) (Memapsin-2).
 GN Name=BACE1; Synonyms=BACE;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20002972; PubMed=10531052; DOI=10.1126/science.286.5440.735;
 RA Vassar R., Bennett B.D., Babu-Khan S., Kahn S., Mendiaz E.A.,
 RA Denis P., Teplow D.B., Rose S., Amarante P., Loeloff R., Luo Y.,
 RA Fisher S., Fuller J., Edenson S., Lile J., Jarosinski M.A.,
 RA Biere A.L., Curran E., Burgess T., Louis J.-C., Collins F.,
 RA Treanor J., Rogers G., Citron M.,
 RA "Beta-secretase cleavage of Alzheimer's amyloid precursor protein by
 RT the transmembrane aspartic protease BACE.";
 RL Science 286:735-741(1999).
 RN [2]
 RP REVISIONS TO 6 AND 81-87.
 RA Bennett B.D., Vassar R., Citron M.,
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;

RA van R., Binkowski M.J., Shuck M.E., Miao H., Terry M.C., Pauley A.M.,
 RA Braahier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity." ;
 RL Nature 402:533-537(1999).
 (4)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogiwa D., Quackenbush J.,
 RA Baladrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Belseri K.W.,
 RA Blake J.A., Brad D., Brusic V., Ciothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedziarski R.M., Kling B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltsev K., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Raveai T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada M.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
 RA Hara A., Hashikume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs." ;
 RL Nature 420:563-573(2002).
 (5)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Gronow L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko U., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.S., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hylk S.W.,
 RA Villalon D., Muzny D.M., Sodergren E.J., Lu X., Gibbs B.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 -1- FUNCTION: Responsible for the proteolytic processing of the
 amyloid precursor protein (APP). Cleaves at the amino termini of
 the A-beta peptide sequence, between residues 671 and 672 of APP,
 leads to the generation and extracellular release of beta-cleaved
 soluble APP, and a corresponding cell-associated carboxy-terminal
 fragment which is later released by gamma-secretase (By
 similarity).
 -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 Val-Leu-Ile-Asp-Ala-Glu-Phe in the Swedish variant of
 Alzheimer's amyloid precursor protein.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- SIMILARITY: Belongs to the peptidase A1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, AF190726; AAF04143.2; -
 CC EMBL, AF200346; AAF17082.1; -
 CC EMBL, AK014464; BAB29370.1; -
 CC EMBL, BC048189; AAB48189.1; -
 CC HSSP, P56817; IM4H.
 CC MEROPS, A01.004; -
 CC MGD: MGI:1346542; Bace1.
 CC InterPro, IPR009119; Pept_A1_BACE.
 CC InterPro, IPR009120; Pept_A1_BACE1.
 CC InterPro, IPR001969; Pept_Asp_AS.
 CC InterPro, IPR009007; Pept_AspArtic.
 CC InterPro, IPR001461; Peptidase_A1.
 CC Pfam, PF00026; Asp; 1.
 CC PRINTS, PR01816; BACE1.
 CC PRINTS, PR01815; BACEFAMILY.
 CC PRINTS, PR00792; PEPSTN.
 CC PROSITE, PS00441; ASP_PROTEASE; 1.
 CC Aspartyl protease; Glycoprotein; Hydroxylase; Signal; Transmembrane;
 CC Zymogen.
 CC KX
 CC FT SIGNAL 1 21 Potential.
 CC FT PROPEP 22 45 Potential.
 CC FT CHAIN 46 501 Beta-secretase 1.
 CC FT DOMAIN 22 457 Extracellular (Potential).
 CC FT TRANSMEM 458 478 Potential.
 CC FT DOMAIN 479 501 Cytoplasmic (Potential).
 CC FT ACT_SITE 93 93 By similarity.
 CC FT ACT_SITE 289 289 By similarity.
 CC FT DISULFID 216 420 By similarity.
 CC FT DISULFID 278 443 By similarity.
 CC FT DISULFID 330 380 By similarity.
 CC FT CARBOHYD 153 153 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 223 223 N-linked (GlcNAc...) (Potential).
 CC FT CARBOHYD 354 354 N-linked (GlcNAc...) (Potential).
 CC FT SEQUENCE 501 AA; 55747 MW; C085A013145B474E CRC64;
 Query Match 96.9%; Score 2216; DB 1; Length 501;
 Best Local Similarity 96.5%; Pred. No. 6; 9e-170;
 Matches 418; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
 Oy 1 THGIRLPRLRSGLGAPLGLINLTDEEPEEPRGRGRSFVENVMDLNRGSGGYVEMTV 60
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 22 THGIRLPRLRSGLGAPLGLRLPRETDESEPRGRGRSFVENVMDLNRGSGGYVEMTV 81
 Oy 61 GSPPTLNLIVDTGSSNFAVGAAPHPFLRRYQRLSSTYRDLRKVVYPTQKKEGL 120
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 82 GSPPTLNLIVDTGSSNFAVGAAPHPFLRRYQRLSSTYRDLRKVVYPTQKKEGL 141
 Oy 121 GTDVLNIPHPNVTYPAANLAITTESKPFINSNMEGLGLVAYIARPDSDLEPFDSL 180
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 142 GTDVLNIPHPNVTYPAANLAITTESKPFINSNMEGLGLVAYIARPDSDLEPFDSL 201
 Oy 181 VQOTHPNLFSLQCGAGFPLNQSEVTLASVGSMIIGGIDHSLYTGSLLWYTPIRREWYE 240
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 202 VQOTHPNLFSLQCGAGFPLNQSEVTLASVGSMIIGGIDHSLYTGSLLWYTPIRREWYE 261
 Oy 241 VIVRVEINGQDLKMDCKEYNTDKSVDSGTTNLRPKVFPFAVAKSIRAASTKFPDG 300
 |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 262 VIVRVEINGQDLKMDCKEYNTDKSVDSGTTNLRPKVFPFAVAKSIRAASTKFPDG 321
 Oy 301 FVLGBOVLVCMQACTTWMNIFPVISLYLWGEVTVNQSRITLPPQVLRPVEDVATSQDDCY 360

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Db      322 FHLGBOVCWQAGTTPMNI.FPVISLYLMGEVNTOSFRITLIPQOYLREVEVATISQDDCY 381
Qy      361 KRAISQSGTGTWGAIVMEGYVFPDRAKRIIGFAVSACHVDEFRITAAVGEFVTLDM 420
Db      382 KRAVSQSSGTGTWGAIVMEGYVFPDRAKRIIGFAVSACHVDEFRITAAVGEFVTLDM 441
Qy      421 DCGYNIPTDEST 433
Db      442 DCGYNIPTDEST 454

RESULT 5
Q8C7R1 PRELIMINARY; PRT: 501 AA.
AC Q8C7R1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2004 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
DE enriched library, clone: C530008K17 product: beta-51te APP cleaving
DE enzyme, full insert sequence.
GN Name=Bace1; Synonym=Bace;
OS Mus musculus (Mouse);
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=92279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaibiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubara S.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spinal cord;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
RA Fukuda S., Futano M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu M., Hiramoto K., Hirooka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Koda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: Belongs to peptidase family A1.
DR EMBL; AK049626; BAC33844.1; -.
DR HSSP; P56817; 1PRN.
DR MCD; MGI:1346542; Bace1.
DR GO; GO:0005768; C:endosome; ISS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005794; C:Golgi apparatus; ISS.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0004130; F:aspartic-type endopeptidase activity; ISS.
DR GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR InterPro; IPR001461; Peptidase A1.
DR InterPro; IPR009119; Pept_A1_BACE1.
DR InterPro; IPR009120; Pept_A1_BACE1.
DR InterPro; IPR009007; Pept_AspArtic.
DR PRINTS; PRO1816; BACE1.
DR PRINTS; PRO1815; BACE1.
DR PRINTS; PRO0792; PEPsin.
DR PROSITE; PS00141; Asp_PROTEASE; 1.
KW Aspartyl protease; Hydrolase; Protease.
SQ SEQUENCE 501 AA; 55761 MW; B410DAB64647663 CRC64;

Query Match 96.8%; Score 2215; DB 2; Length 501;
Best Local Similarity 96.3%; Pred. No. 8.3e-170;
Matches 417; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy      1 TOHGIRLPLRSGLGAPLGLIEINLEFDEEPEEGRGSPFVENVDLRGSGGQYVENV 60
Db      22 THGIRLPLRSGLAGPLGLRLPRETDESEEPGRGSPFVENVDLRGSGGQYVENV 81
Qy      61 GSPPTLNLIVDTGSSNFVGAAPHLHRYQRLSSTYRDLRGVYVPTQGMGEGEL 120
Db      82 GSPPTLNLIVDTGSSNFVGAAPHLHRYQRLSSTYRDLRGVYVPTQGMGEGEL 141
Qy      121 GTPLVSIIPHPNVTYRANIAITSDKPFINSNNEGILGLAYAIAPDDSLPEFPDSL 180
Db      142 GTPLVSIIPHPNVTYRANIAITSDKPFINSNNEGILGLAYAIAPDDSLPEFPDSL 201
Qy      181 VQOTHPNLFSLQCGAPPLNQSEVLASVGSMTIGIDISLVTGSLMTYPIRREWE 240
Db      202 VQOTHPNLFSLQCGAPPLNQTEALASVGSMTIGIDISLVTGSLMTYPIRREWE 261
Qy      241 VTIIVEINGDGLKMDCKEYNDKSIYDSGTTNLRPKVEAAVKSIIKAASSTKPEPDG 300
Db      262 VTIIVEINGDGLKMDCKEYNDKSIYDSGTTNLRPKVEAAVKSIIKAASSTKPEPDG 321
Qy      301 FHLGBOVCWQAGTTPMNI.FPVISLYLMGEVNTOSFRITLIPQOYLREVEVATISQDDCY 360
Db      322 FHLGBOVCWQAGTTPMNI.FPVISLYLMGEVNTOSFRITLIPQOYLREVEVATISQDDCY 381
Qy      361 KRAISQSGTGTWGAIVMEGYVFPDRAKRIIGFAVSACHVDEFRITAAVGEFVTLDM 420
Db      382 KRAVSQSSGTGTWGAIVMEGYVFPDRAKRIIGFAVSACHVDEFRITAAVGEFVTLDM 441
Qy      421 DCGYNIPTDEST 433
Db      442 DCGYNIPTDEST 454

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RESULT 6
 Q8BOY4 PRELIMINARY; PRT; 501 AA.
 AC Q8BOY4
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
 DE enriched library, clone:8230346M13 product:beta-site APP cleaving
 DE enzyme, full insert sequence.
 GN Name=Bace1; Synonyms=Bace;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carinci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA The PANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=2050913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoa T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasubawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numasaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Teganai M.,

RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family A1.
 DR EMBL; AK046175; BAC32620.1; -.
 DR HSSP; P56817; 1FKN.
 DR MGD; MGI:1346542; Bace1.
 DR GO; GO:0005768; C:endosome; ISS.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0005794; C:Golgi apparatus; ISS.
 DR GO; GO:0016021; C:integral to membrane; ISS.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
 DR GO; GO:0050435; P:beta-amyloid metabolism; ISS.
 DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009119; Pept_A1_BACE.
 DR InterPro; IPR009120; Pept_A1_BACE.
 DR InterPro; IPR009007; Pept_Aspartic.
 DR InterPro; IPR01969; Pept_Asp_AS.
 DR PRINTS; PR01816; BACE1.
 DR PRINTS; PR01815; BACEFAMILY.
 DR PRINTS; PR00792; PEPSTN.
 DR PROSITE; PS00141; ASP_PROTEASE, 1.
 DR Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 501 AA; 55816 MW; C085513145B024E CRC64;
 Query Match 96.6%; Score 2211; DB 2; Length 501;
 Best Local Similarity 96.3%; Pred. No. 1,7e-163;
 Matches 417; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 1 TQHGIRLPFRSGLGAPLGLIEINLTDEEPEPEGRGSGFVEMVDNLRKSGGQYVEMTV 60
 DB 22 THLGRLPFRSLAPPLGLRPRETDESEEPGRGSGFVEMVDNLRKSGGQYVEMTV 81
 QY 61 GSPPTNLIVDTGSSNFAVGAAPFLHRYRQLSSTYRDLRGVYVPTQGWEGEL 120
 DB 82 GSPPTNLIVDTGSSNFAVGAAPFLHRYRQLSSTYRDLRGVYVPTQGWEGEL 141
 QY 121 GTDLVSIHPGPNVTVRANIAATTESDKFFINSNMEGILGLAYATARPDDSLPPFSL 180
 DB 142 GTDLVSIHPGPNVTVRANIAATTESDKFFINSNMEGILGLAYATARPDDSLPPFSL 201
 QY 181 VQOTHPNPLFSQLGAGPPLNQSSEVLASVGSMTIIGIDHSLYTGSLMYTPIRREWYE 240
 DB 202 VQOTHPNPLFSQLGAGPPLNQSSEVLASVGSMTIIGIDHSLYTGSLMYTPIRREWYE 261
 QY 241 VTIIVEINGQDLKMDCKEYNDKSIIVDSGTTNLRPKVFEAAVKSIIKAASTKEFPDG 300
 DB 262 VTIIVEINGQDLKMDCKEYNDKSIIVDSGTTNLRPKVFEAAVKSIIKAASTKEFPDG 321
 QY 301 FWLGEOLVQWAGTTPWNIFFVITSLYLMGEVTNOSFRITILPQOYLRPVEDVATGDDCY 360
 DB 322 FWLGEOLVQWAGTTPWNIFFVITSLYLMGEVTNOSFRITILPQOYLRPVEDVATGDDCY 381
 QY 361 KRAISGSSGTMGAVIMEGFVVDPRAKRIGFVPSACHVDEFTAAVEGPFYTLDME 420
 DB 382 KRAVSSGSSGTMGAVIMEGFVVDPRAKRIGFVPSACHVDEFTAAVEGPFYTLDME 441
 QY 421 DCGYNIPTDDEST 433
 DB 442 DCGYNIPTDDEST 454
 RESULT 7
 Q9UUS1 PRELIMINARY; PRT; 532 AA.
 AC Q9UUS1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE KIAA1149 protein (Fragment).
 GN Name=KIAA1149;
 OS Homo sapiens (human).

OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
RN	NCB1_textid=9606;
RP	(1)
RC	SEQUENCE FROM N.A.
RA	TISSUE=Brain;
RX	MEDLINE=20039618; PubMed=1074461;
RT	Hitoosawa M., Nagase T., Iehikawa K., Kikuno R., Nomura N., Ohara O.,
RL	"Characterization of cDNA clones selected by the Genetrix analysis from size-fractionated cDNA libraries from human brain."; DNA Res. 6:329-336(1999).
CC	-1 SIMILARITY: Belongs to peptidase family A1.
DR	EMBL; AB032975; BAA8463.2; -.
DR	HSSP; P56817; IPKN.
DR	GO; GO:0005768; C:endosome; ISS.
DR	GO; GO:0005794; C:Golgi apparatus; ISS.
DR	GO; GO:0016021; C:integral to membrane; ISS.
DR	GO; GO:0004190; F:aspartic-type endopeptidase activity; ISS.
DR	GO; GO:0050435; P:beta-amyloid metabolism; ISS.
DR	GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
DR	InterPro; IPR001463; Peptidase_A1.
DR	InterPro; IPR009119; Pept_A1_BACE.
DR	InterPro; IPR009120; Pept_A1_BACE1.
DR	InterPro; IPR009007; Pept_Aspatic.
DR	InterPro; IPR001969; Pept_Asp_AS.
DR	PRINTS; PRO1816; BACE1.
DR	PRINTS; PRO1815; BACEFAMILY.
DR	PRINTS; PRO0792; PEPSIN.
DR	PROSITE; PS00141; ASP_PROTEASE; 1.
KW	Apartyl protease; Hydrolase; Protease.
FT	NON_TER
SQ	SEQUENCE 532 AA; 58720 MW; 98B135DD5FBD28 CRC64;

QY	6	PLRSLGAGAPLGLIETLEETDEEBEERGRGSFEVEMVDNLGRKSGGGYVEMTVGSPQOTL	67
Db	60	PCAAWGAAPLGLRLPRETDEEBEERGRGSFEVEMVDNLGRKSGGGYVEMTVGSPQOTL	119
QY	68	NILVDTGSSNFAVGAAHPFELHRRYQOROLSTYRDLRGVVYPTQGMKEGLGTDLYSI	127
Db	120	NILVDTGSSNFAVGAAHPFELHRRYQOROLSTYRDLRGVVYPTQGMKEGLGTDLYSI	179
QY	128	PHGPVTVYRANIAAITESDKPFINGSNMEGLIGLVAEILARDDSLBEPFSLVQTHVP	187
Db	180	PHGPVTVYRANIAAITESDKPFINGSNMEGLIGLVAEILARDDSLBEPFSLVQTHVP	239
QY	188	NLFSLOLCGAGPPLNOSEVLASVGSMTIGGIDHSLTYGSLMYTPIRREMYEYIYAVE	247
Db	240	NLFSLOLCGAGPPLNOSEVLASVGSMTIGGIDHSLTYGSLMYTPIRREMYEYIYAVE	299
QY	248	INGODLXMDCKEYNDKSIYVDSGTLNLRPKKVFPAAYKSIKAASTFKPFDGFWLGBOL	307
Db	300	INGODLXMDCKEYNDKSIYVDSGTLNLRPKKVFPAAYKSIKAASTFKPFDGFWLGBOL	359
QY	308	VCMQAGTTPMNIIPYISLYMGEVYNOSFRITLIPQYLREVEVYASODDCYFAISQS	367
Db	360	VCMQAGTTPMNIIPYISLYMGEVYNOSFRITLIPQYLREVEVYASODDCYFAISQS	419
QY	368	STGTVMGAVINEGFVYVDFRARKRIGFVASCYHDEERTAAVSGPVTLLDMEDCGYNIP	427
Db	420	STGTVMGAVINEGFVYVDFRARKRIGFVASCYHDEERTAAVSGPVTLLDMEDCGYNIP	479
QY	428	QTDEST 433	
Db	480	QTDEST 485	

AC ORC4F4
DT 01-MAR-2003 (TREMBlRel. 23. Created)
DT 01-MAR-2003 (TREMBlRel. 23. Last sequence update)
DT 01-MAR-2004 (TREMBlRel. 26. Last annotation update)
DE Mus musculus o day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:IC230037E16 product:beta-site APP cleaving enzyme, full length sequence.
DE DE
GN Name=Bacel; Synonym=Bace;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI|Entrez|10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=2108560; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
RL [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komio H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
RL [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shihata K., Itoh M., Atzawa K., Nagoka S., Sasaki N., Carninci P., Suni N., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh W., Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kasaiwa K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wachihi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawaji U., Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multiplexed sequencer."; Genome Res. 10:1757-1771(2000).
RL [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX Adachi V., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Henagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiyaoka T., Hirozane T., Horii F., Imotani K., Ishii Y., Itoh W., Kagawa T., Kanokawa T., Katoh H., Kawai Y., Kojima Y., Kondo S., Komio H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y., Saeki D., Shibata K., Sakai C., Sakai K., Sakazume N., Sano H., Sasagi A., Takahashi F., Takearu-Akaiwa S., Takada Y., Tagami M., Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toy T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (Apr-2002) to the EMBL/GenBank/DDJB databases.
RL -1- SIMILARITY: Belongs to the peptidase family A1.

DR EMBL; AK082317; BAC38462.1; --
 DR HSSP; P56817; IPRN.
 DR MGD; MGI:1346542; Bace1.
 DR GO; GO:0005768; C-endosome; ISS.
 DR GO; GO:0005615; C-extracellular space; TMS.
 DR GO; GO:0005794; C-integral to membrane; ISS.
 DR GO; GO:0016021; C-integral to membrane; ISS.
 DR GO; GO:0004190; F-aspartic-type endopeptidase activity; ISS.
 DR GO; GO:0050435; F-beta-amyloid metabolism; ISS.
 DR GO; GO:0005509; P-membrane protein ectodomain proteolysis; ISS.
 DR InterPro; IPR001461; Peptidase A1.
 DR InterPro; IPR009119; Pept_A1_BACE.
 DR InterPro; IPR009120; Pept_A1_BACE.
 DR InterPro; IPR009007; Pept_Aspartic.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR PRINTS; PRO1816; BACE1.
 DR PRINTS; PRO1815; BACEFAMILY.
 DR PRINTS; PRO0792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 DR Aspartyl protease; Hydrolyase; Protease.
 KW ASpartyl protease; Hydrolyase; Protease.
 SQ SEQUENCE 467 AA; 52063 MW; 31AB674F1843652 CRC64;

Query Match 88.4%; Score 2023; DB 2; Length 467;
 Best Local Similarity 88.7%; Pred. No. 2,2e-154; Indels 34; Gaps 1;
 Matches 384; Conservative 5; Mismatches 10;

QY 1 TGHGIRLPARGSLGAPLGLINLETDEPERPGRGSEFVENVNLRKSGGGYVEMTV 60
 DB 22 TLHGIRLPARGSLGAPLGLRLPRETDESEBERGRGSEFVENVNLRKSGGGYVEMTV 81
 QY 61 GSPPTQNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRKGVYVPTQKKEGL 120
 DB 82 GSPPTQNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRKGVYVPTQKKEGL 141
 QY 121 GRDIVSIHPGPNVTYRANITATSESKPFINSNMGIGLVAETARDDSLPEPFDL 180
 DB 142 GRDLVSIHPGPNVTYRANITATSESKPFINSNMGIGLVAETARDDSLPEPFDL 201
 QY 181 VQKTHVPLNFSIQLCGAGFPLNQEVLASVSGSMITGIDHSIYTSGLWYTPIRRMWYE 240
 DB 202 VQKTHVPLNFSIQLCGAGFPLNQEVLASVSGSMITGIDHSIYTSGLWYTPIRRMWYE 261
 QY 241 VTIIRVEINGODLKMDCKEYNYDKSIVDSGTTNLRPKVFEAAVKSIRAASTKPPDG 300
 DB 262 VTIIRVEINGODLKMDCKE-----TEKPPDG 287
 QY 301 FNLGEBLVYCWQAGTTTWNIPVVISLXMGVYTNOSFRITLPOOYLRPVEDVATSDDDCY 360
 DB 288 FNLGEBLVYCWQAGTTTWNIPVVISLXMGVYTNOSFRITLPOOYLRPVEDVATSDDDCY 347
 QY 361 KFAISQSTGTWAGVIMGFYVFPDRAKRIRIGFAVSACHVHDEFRTAAVEGPFVTLDM 420
 DB 348 KFAVSQSTGTWAGVIMGFYVFPDRAKRIRIGFAVSACHVHDEFRTAAVEGPFVTLDM 407
 QY 421 DCGYNIPTDEST 433
 DB 408 DCGYNIPTDEST 420
 RESULT 9
 ID Q6NZT7 PRELIMINARY; PRT; 505 AA.
 AC Q6NZT7;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 GN Hypothetical protein zgc:77409.
 GN Namezgc:77409;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 OX

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Kuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RC Director MGC Project;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family A1.
 DR EMBL; BC065973; AAH65973.1; --
 DR HSSP; P56272; IAMS.
 DR ZFIN; ZDB-GENE-040426-1835; zgc:77409.
 DR GO; GO:0009049; F-aspartic-type signal peptidase activity; IEA.
 DR GO; GO:0004194; F-pepsin A activity; IEA.
 DR GO; GO:0008233; F-peptidase activity; IEA.
 DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001461; Peptidase A1.
 DR InterPro; IPR009119; Pept_A1_BACE.
 DR InterPro; IPR009120; Pept_A1_BACE.
 DR InterPro; IPR009007; Pept_Aspartic.
 DR InterPro; IPR001969; Pept_Asp_AS.
 DR PRINTS; PRO1816; BACE1.
 DR PRINTS; PRO1815; BACEFAMILY.
 DR PRINTS; PRO0792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 1.
 KW Aspartyl protease; Hydrolyase; Hypothetical protein; Protease.
 SQ SEQUENCE 505 AA; 55661 MW; 6C83D4ACFD903BAD CRC64;

Query Match 78.4%; Score 1794; DB 2; Length 505;
 Best Local Similarity 77.3%; Pred. No. 7.1e-136; Indels 12; Gaps 3;
 Matches 338; Conservative 40; Mismatches 47;

QY 5 IRLPRLSGAGPLGLEINLETDEPERPGRG-----SFENVNLRKSGGGYV 57
 DB 28 IRLPRLSGAGPLGLEINLETDEPERPGRG-----SFENVNLRKSGGGYV 83
 QY 58 MTGSPPTQNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRKGVYVPTQKKE 117
 DB 84 MAVGSPAQRLNIVDTGSSNFVGAAPHPFLHRYRSLSSYRDLGRGVYVPTQGRWE 143
 QY 118 GELGDLVSIHPGPNVTYRANITATSESKPFINSNMGIGLVAETARDDSLPEPFDL 177
 DB 144 GELGDLVSIHPGPNVTYRANITATSESKPFINSNMGIGLVAETARDDSLPEPFDL 203
 QY 178 DSLVQKTHVPLNFSIQLCGAGFPLNQEVLASVSGSMITGIDHSIYTSGLWYTPIRRM 236
 DB 204 DSLVQKTHVPLNFSIQLCGAGFPLNQEVLASVSGSMITGIDHSIYTSGLWYTPIRRM 263
 QY 237 WYEVVIVVEINGODLKMDCKEYNYDKSIVDSGTTNLRPKVFEAAVKSIRAASTK 296
 DB 264 WYEVVIVVEINGODLKMDCKEYNYDKSIVDSGTTNLRPKVFEAAVKSIRAASTK 323

Qy 297 FPDGFWLGEOLNOMAGTTPMNIIPVISTYLMGEVNTGSPFRITITLPOQYLAREVEDVATSO 356
Db 324 FPGGFWLGEOLNOMAGTTPMNIIPVISTYLMSENNOFSRISITLPOQYLAREVEDVATSO 383
Qy 357 DDCYKFAISQSSGTGTMGAVIMEGFYVFPDRAKRIKIGFVASCYHNDERRRAVGEPPVT 416
Db 384 EDCYKFAVSSQSSGTGTMGAVIMEGFYVFEROKHIGFVASTCHVHDEFTAAVGEPPHG 443
Qy 417 LDMEDCGYNIPOQDEST 433
Db 444 LDMEDCGYNIPOQDEST 460

RESULT 10

Q99206 PRELIMINARY; PRT; 373 AA.
AC 099206: 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE MKIA1149 protein (Fragment).
GN Name=MKIA1149;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RA Okazaki N., Kikuno R.P., Ohara R., Inamoto S., Koseki H., Hirooka S.,
Saga Y., Seino S., Nishimura M., Katsuo T., Hoshino K., Kitamura H.,
Nagase T., Ohara O., Koga H.,
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11.205-218(2004).
DR EMBL: AK173112; BAD32390.1;
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR001461; Peptidase_A1.
DR InterPro: IPR009120; Pept_A1_BACE1.
DR InterPro: IPR009007; Pept_Aspartic.
DR PRINTS: PRO1816; BACE1.
DR PRINTS: PRO0792; PEPSTN.
FT NON TER 1
SQ SEQUENCE 373 AA; 41710 MW; 9D7D19D039577732 CRC64;

Query Match 74.8%; Score 1711; DB 2; Length 373;
Best Local Similarity 98.2%; Pred. No. 2.3e-129;
Matches 320; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 108 YVPYTGKKEGELDTLVSIPIHGPVTVTANIAITTESDKPFINSNMEGILGLAVAEIA 167
Db 1 YVPYTGKKEGELDTLVSIPIHGPVTVTANIAITTESDKPFINSNMEGILGLAVAEIA 60
Qy 168 RPDSDLEPPFDSLVTQTHVPLNFSIQLGAGPPLNQSVLAVSGSMITIGIDHSITVGS 227
Db 61 RPDSDLEPPFDSLVTQTHVPLNFSIQLGAGPPLNQSVLAVSGSMITIGIDHSITVGS 120
Qy 228 LMYTIRREMYEVIIIVAEINGQDLKMDCKEYNDKSIYDSTTNLRLPKVEAAVKS 287
Db 121 LMYTIRREMYEVIIIVAEINGQDLKMDCKEYNDKSIYDSTTNLRLPKVEAAVKS 180
Qy 288 IKAASSTKFPDGFALGEOLNOMAGTTPMNIIPVISTYLMGEVNTGSPFRITITLPOQYL 347
Db 181 IKAASSTKFPDGFALGEOLNOMAGTTPMNIIPVISTYLMGEVNTGSPFRITITLPOQYL 240
Qy 348 FVEVDVATSOQDCYKFAISQSSGTGTMGAVIMEGFYVFPDRAKRIKIGFVASCYHNDERR 407
Db 241 FVEVDVATSOQDCYKFAISQSSGTGTMGAVIMEGFYVFPDRAKRIKIGFVASCYHNDERR 300
Qy 408 AAVEGPFVTLDMEDCGYNIPOQDEST 433

Db 301 AAVEGPFVTLDMEDCGYNIPOQDEST 326

RESULT 11

Q9CUC5 PRELIMINARY; PRT; 267 AA.
AC 09CUC5: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 23, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Mus musculus adult male brain cDNA, RIKEN full-length enriched
DE library, clone:3526402A15 Product:beta-site APP cleaving enzyme, full
DE insert sequence. (Fragment).
GN Name=Bace1; Synonyms=Bace;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komori H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shihata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komori H., Akiyama J., Nishi K., Kitsuura T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa K., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
RA Yoneda Y., Ishikawa T., Inoue Y., Kira A., Hayashizaki Y.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RA Aichi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Haraoka T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imatani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komori H., Kouda M., Koya S., Kuzuhara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Mutamatsu M., Hayashizaki Y.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK014390; BAB29317.2; -.
 DR HSSP; P56817; 1FKN.
 DR MGD; MG1:1346542; Bace1.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR009120; Repc_A1_BACE1.
 DR InterPro; IPR009007; Repc_Aspartic.
 DR PRINTS; PRO1816; BACE1.
 DR FT NON TER 1 1
 SQ SEQUENCE 267 AA; 3033 MW; 9413E84530AB63B0 CRC64;
 Query Match 50.8%; Score 1163; DB 2; Length 267;
 Best Local Similarity 99.1%; Pred. No. 2,1e-85;
 Matches 218; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 214 MIIIGDHSLYTSGSLTYTTPIRREMYEVIIVRIINGQDLKMDCKEYNDKSIYDSGTTN 273
 DB 1 MIIIGDHSLYTSGSLTYTTPIRREMYEVIIVRIINGQDLKMDCKEYNDKSIYDSGTTN 60
 QY 274 LRLPKVFEAFAVKSIAKASTKPEPDGFMVGEQVCMQAGTTPWNIIPVISTLYMGEVTN 333
 DB 61 LRLPKVFEAFAVKSIAKASTKPEPDGFMVGEQVCMQAGTTPWNIIPVISTLYMGEVTN 120
 QY 334 QSFRRITLLPQGYRPEVDVATSDDDCKFAISGSSGTGTWGANVIMGFFVYPPRAKRIG 393
 DB 121 QSFRRITLLPQGYRPEVDVATSDDDCKFAISGSSGTGTWGANVIMGFFVYPPRAKRIG 180
 QY 394 FANSACHVDEPRTAIVEGPFVTLMDGCGYNIPQIDEST 433
 DB 181 FANSACHVDEPRTAIVEGPFVTLMDGCGYNIPQIDEST 220

RESULT 12
 BAE2_HUMAN STANDARD; PRT; 518 AA.
 ID BAE2_HUMAN STANDARD; PRT; 518 AA.
 AC Q9Y5Z0; Q9UT6;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Beta secretase 2 precursor (BC 3.4.23.45) (Beta-site App-cleaving
 DE enzyme 2) (Aspartyl protease 1) (Asp 1) (ASPL) (Membrane-associated
 DE aspartic protease 1) (Memapsin-1) (Down region aspartic protease)
 DE (UNQ418/PRO852).
 GN Name=BACE2; Synonyms=ASP21;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
 RA Yan R., Bienkowski M.J., Shuck M.E., Miao H., Torg M.C., Paulley A.M.,
 RA Braisher J.R., Strachan N.C., Mathews W.R., Buhl A.E., Carter D.B.,
 RA Tomaselli A.G., Parodi L.A., Heinrichson R.L., Garney M.E.;
 RT "Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 RT secretase activity.";
 RL Nature 402:533-537(1999).
 RN 12)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Xin H., Stephens J.C., Duan X., Harrowe G., Kim E., Grieshammer U.,
 RT "Identification of a novel aspartic-like protease differentially
 RT expressed in human breast cancer cell lines.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN 13)
 RP SEQUENCE FROM N.A.

RA Accarino M.P., Pumagalli P., Ottolenghi S., Taramelli R.;
 RT "Cloning of a gene from chromosome 21 Down region encoding a potential
 RT transmembrane aspartyl protease.";
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN 14)
 RP SEQUENCE FROM N.A.
 RA Solans A., Estivill X., de la Luna S.;
 RT "Cloning of a novel mammalian aspartyl protease.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN 15)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811;
 RA Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D.,
 RA Chapman C., Gloger I.S., Murphy K.E., Southern C.D., Ryan D.M.,
 RA Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.;
 RT "Identification of a novel aspartic proteinase (Asp 2) as beta-
 RT secretase.";
 RL Mol. Cell. Neurosci. 14:419-427(1999).
 RN 16)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2014060; PubMed=10677483; DOI=10.1073/pnas.97.4.1456;
 RA Lin X., Koelsch G., Wu S., Downs D., Dantli A., Tang J.;
 RT "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 RT beta-amyloid precursor protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 RN 17)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22887396; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gunney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Roeder J., Grimaldi C., Gu Q., Haas P.B., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robble E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Wleand D., Woode K., Xie M.-H., Yanura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN 18)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
 RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
 RA Reichwald A., Rump A., Shillhabel M., Schudy A., Zimmermann W.,
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
 RA Shintani A., Sasaki T., Nagamine K., Mitsuhashi S., Antonarakis S.E.,
 RA Minoshima S., Shimizu N., Nordstok G., Hornischer K., Brandt P.,
 RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
 RA Ramser J., Beck A., Klages S., Hennig S., Riessmann L., Dagand B.,
 RA Wehnemeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
 RA Leirich H., Reinhardt R., Yaspo M.-L.;
 RT "The DNA sequence of human chromosome 21.";
 RL Nature 405:311-319(2000).
 RN 19)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Krausner R.D., Collins L., Wagner F.S., Wagner C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heifetz F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abrahams R.D., Mullaly S.J.,
 RA Bosak S.A., McKean P.J., McKernan K.J., Malek A.M., Gundaretan P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shechenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [10]
 RP CHARACTERIZATION.
 RX MEDLINE:22088158; PubMed:12093293; DOI=10.1021/bi025926t;
 RA Turner R.T. III, Loy J.A., Nguyen C., Devaasudram T., Ghosh A.K.,
 RA Koelsch G., Tang J.,
 RT "Specificity of memapsin 1 and its implications on the design of
 RT memapsin 2 (beta-secretase) inhibitor selectivity.";
 RL Biochemistry 41:8742-8746(2002).
 CC -1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-
 CC Val-Aen-Leu-1-Asp-Ala-Glu-Phe in the Swedish variant of
 CC Alzheimer's amyloid precursor protein.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Belongs to the peptidase A1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AF200342; AAF17078.1; -
 DR EMBL; AF117892; AAD45240.1; -
 DR EMBL; AF050171; AAD45963.1; -
 DR EMBL; AF178532; AAF29494.1; -
 DR EMBL; AF204944; AAF26368.1; -
 DR EMBL; AF200192; AAF13714.1; -
 DR EMBL; AY358927; AAO89286.1; -
 DR EMBL; AL163284; CAB90458.1; -
 DR EMBL; BC014453; CAB90554.1; -
 DR HSSP; P56817; 1M4H.
 DR MEROPS; A01.041; -
 DR Genew; HGNC:934; BACE2.
 DR MIM; 605668; -
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.
 DR GO; GO:0006464; P:protein modification; TAS.
 DR GO; GO:0009306; P:protein secretion; TAS.
 DR InterPro; IPR009119; Pept_A1_BACE.
 DR InterPro; IPR009121; Pept_A1_BACE2.
 DR InterPro; IPR009007; Pept_Asp_AS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR Pfam; PF00026; Asp_1.
 DR PRINTS; PRO1817; BACE2.
 DR PRINTS; PRO1815; BACEFAMILY.
 DR PROSITE; PRO0792; PEPsin.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 DR Aspartyl protease; Glycoprotein; Hydrolase; Signal; Transmembrane;
 KW Zymogen.
 FT SIGNAL 1 20 Potential.
 FT PROPEP 21 ? Potential.
 FT CHAIN 21 518 Beta secretase 2.
 FT DOMAIN 21 473 Extracellular (Potential).
 FT TRANSMEM 474 494 Potential.
 FT DOMAIN 495 518 Cytoplasmic (Potential).
 FT ACT_SITE 110 110 By similarity.
 FT ACT_SITE 303 303 By similarity.
 FT CARBOHYD 170 170 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 366 366 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 36 36 A -> T (in Ref. 6).
 SQ SEQUENCE 518 AA; 56180 MW; 28903150823760D3 CRC64;

Query Match 49.7%; Score 1136; DB 1; Length 518;
 Best Local Similarity 52.2%; Pred. No. 7,8e-83;
 Matches 215; Conservative 66; Mismatches 121; Indels 10; Gaps 3;
 QY 8 PLRSLGAGPLGLINLETDERPEPCGRGSRFVEMVDNLRGKSGQGVVENTVSGPOTL 67
 DB 52 PARRHADGIALALEPALAS-----PAGANPFLMVDNLQDSRGTYLEMLIGTPQKL 105
 QY 68 NILVDTGSSNFAVGAAHPFLHRYQROLSTYDRLKRGVVPYTGKMBGLCTDLVSI 127
 DB 106 QLVDTGSSNFAVGAPTPSYIDTYFDTERSTYSKSGFDVTVKYGQSGMTGFGVEDLVTI 165
 QY 128 PRGPVTVRANIAATTESDKEFNGSNWEGILGAAYEARPPDSLEPPFDSLVKQTHVP 187
 DB 166 PKGFPTSLVNIATIFESENFPLGIKNGILGAIYVTLKAPSSLETFFDSLVTOANIP 225
 QY 168 NLFSLQCGAGPPLNQSEVLASVGSMTIGGIDHSILYTSGLWYTPIRREWYEVIIYRV 247
 DB 226 NVFSWQMGAGIPVAGS---GTNGSLVLGGIEPISLYKGIWYTPIKIEWYVYIETLKE 282
 QY 248 INGODLRKMDCKEYVYVDSGFTNLRPKVPEAAVKSIXKASSTKRPDGFMLGEOU 307
 DB 283 IGGSLINDCKEYNADALVDSGTLRLPKQVFDVAVEVARASLIPERSDGFMTGSOUL 342
 QY 308 VCMQAGTPWNI FVVISLYMGVTVNQSPFRITLLPOQYLPVVDVATSGDDCYKFAISOS 367
 DB 343 ACWTNSETPWSPYFKISILYRDENSRSFRITLLPOLYIQPMWAGLANV-ECRFPISFS 401
 QY 368 STGVMGAVIMEGYVYVFDRAARKRIGPAGVACVHBEFTAAVEGFPVTLDM 419
 DB 402 TNALVIGATWEGRYVLEDPARQKRGFPASPACIEAGAAVSEISGPFSTEDV 453
 RESULT 13
 ID Q9H2V8 PRELIMINARY; PRT; 439 AA.
 AC Q9H2V8;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CDA13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pneurocytoma;
 RA Li Y., Huang Q., Peng Y., Song H., Yu Y., Xu S., Ren S., Chen Z.,
 RA Han Z.,
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to peptidase family A1.
 DR EMBL; AF212252; AAG41783.1; -
 DR HSSP; P56817; 1FXN.
 DR GO; GO:0016021; C:integral to membrane; ISS.
 DR GO; GO:0006509; P:membrane protein ectodomain proteolysis; ISS.
 DR GO; GO:0042985; P:negative regulation of amyloid precursor pr...; ISS.
 DR GO; GO:0016486; P:peptide hormone processing; ISS.
 DR InterPro; IPR001461; Peptidase_A1.
 DR InterPro; IPR009119; Pept_A1_BACE.
 DR InterPro; IPR009121; Pept_A1_BACE2.
 DR InterPro; IPR009007; Pept_Asp_AS.
 DR PRINTS; PRO1817; BACE2.
 DR PRINTS; PRO0792; PEPsin.
 DR PRINTS; PRO1815; BACEFAMILY.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 DR PROSITE; PS00141; ASP_PROTEASE; 2.
 DR Aspartyl protease; Hydrolase; Protease.
 SQ SEQUENCE 439 AA; 48275 MW; 02EC0E50F11602 CRC64;
 Query Match 49.0%; Score 1121; DB 2; Length 439;
 Best Local Similarity 54.8%; Pred. No. 1e-81;

Matches 207; Conservative 63; Mismatches 104; Indels 4; Gaps 2;

QY 42 MVDNLKSGGQGYVEMTVGSPQTLNIVDTGSSNFVAGAAPHPFLHRYGRLQSLSTYR 101
 DB 1 MVDNLQSGSGRGVYLEMLIGTPPQKLQIVDTGSSNFVAGAPHPHXYIDTYFPTSSSTYR 60

QY 102 DIRKGVYVYPTGCKKEGELGTLVSPHPNPNTVRAVIAITESDKFPIGNSNMGITL 161
 DB 61 SKGFDVYVYPTGSGWGFGEEDLVITPKGPNISFLVNIITFESSENFPLGKMGITL 120

QY 162 AYAARLPDSDLEPFDSLVKQTHVNLPSLQCGAFPLNOSSEVLAASVGSMTIGGDH 221
 DB 121 AYAATLAKSSLETFFDSLVQANTVNSMOMCGAGLFAAS---GTMGSLVIGGTFP 177

QY 222 SLYTGSMTYPIRREWYEVIIIVRVINGQDLKMDCKEYNYKSIYDSGTTNLRPKYF 281
 DB 178 SLYKGDIVTPIKEBYYQIELKKEIGGSLNLDREYNADKAVDSCTTLRLPQKVF 237

QY 282 EAAVNSIKRAASSTKPPDGFVGLGEOLVCHQAGTTPNITPVISLYMGVNTQSPRITTL 341
 DB 238 DAVEVAVARASLIPFSDGFMTGSQLACWTNSETPWSYFPKISIVLRDMSRSRFRITTL 297

QY 342 PQOYLRPVDAVTSQDDCYKFAISOSTGTWNGAVMEGFYVDFRARRKRGPAVACHV 401
 DB 298 POLYTOPMMGAGLNY-ECYRFGISPSINALVIGATVMEGFYVDFRARRKRGPAVACHV 356

QY 402 HDEFRTAAGEPFTLDM 419
 DB 357 IAGANVSEISGPRSTDV 374

RESULT 14
 Q8CSE9 . PRELIMINARY; PRT; 514 AA.

AC Q8CSE9; 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Mus musculus 15 days embryo male testis cDNA, RIKEN full-length
 DE enriched library, clone:8030470009 product:beta-site APP-cleaving
 DE enzyme 2, full insert sequence.
 GN Name:Bace2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Riken Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium;
 RA the Riken Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=20493934; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Atzawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Atzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Mura M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohse N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- Similarity: Belongs to peptidase family A1.
 DR EMBL: AK078770; BAC37384.1; -
 DR HSSP: P56817; 1PKX.
 DR MEROPS: A01.041; -
 DR MGD: MG1:160440; Bace2.
 DR GO: GO:0005615; C:extracellular space; TMS.
 DR GO: GO:0016021; C:integral to membrane; ISS.
 DR GO: GO:0006509; P:membrane protein ectodomain proteolysis; pr. .; ISS.
 DR GO: GO:0042985; P:negative regulation of amyloid precursor pr. .; ISS.
 DR GO: GO:0016486; P:peptide hormone processing; ISS.
 DR InterPro: IPR001461; Peptidase A1.
 DR InterPro: IPR005119; Pept_A1-BACE.
 DR InterPro: IPR009121; Pept_A1-BACE2.
 DR InterPro: IPR009007; Pept_Aspartic.
 DR InterPro: IPR001969; Pept_Asp_AS.
 DR PRINTS: PRO1817; BACE2
 DR PRINTS: PRO1815; BACSFAMILY.
 DR PRINTS: PRO0792; PEPsin.
 DR PROSITE: PS00141; ASP_PROTEASE; 2.
 DR Aspartyl protease; Hydrolase; Protease.
 KW SQUENCE 514 AA; 55810 MW; CB99237B86A0B2E CRC64;
 SO

Query Match 49.0%; Score 1120; DB 2; Length 514;
 Best Local Similarity 52.5%; Pred. No. 1.5e-81;
 Matches 217; Conservative 67; Mismatches 113; Indels 16; Gaps 6;

QY 12 GIG--GAP--GLEINLTDEDEPERGR-RGSFVEVDVLRGSGGYVEMTVGSPQPT 66
 DB 48 GGTGELPADGIALAL-----EPVRAVNFAMVDVLDQSDSGRGVYLEMLIGTPPK 100

QY 67 LNIIVDTGSSNFVAGAAPHPFLHRYGRLQSLSTYDLRKGVYVYPTGCKKEGELGTLV 126
 DB 101 VOIVDTGSSNFVAGAPHPHXYIDTYFDSSTYSKSGFDVYVYPTGSGWGFGEEDLV 160

QY 127 IPHGPNVTVRAVIAITESDKFPIGNSNMGITLGAAYAIARPDSDLEPFPSVYQTHV 186
 DB 161 IPKGFNSSFLVNIATFESSENFPLGKMGITLGAAYAIARPDSDLEPFPSVLAQAKI 220

QY 187 PNLFSQLCGAPPLNOSSEVLAASVGSMTIGGIDSLYGSMTYPIRREWYEVIIIVRV 246
 DB 187 PNLFSQLCGAPPLNOSSEVLAASVGSMTIGGIDSLYGSMTYPIRREWYEVIIIVRV 246

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2005, 00:26:34 ; Search time 302 Seconds
(without alignment)
2346.052 Million cell updates/sec

Title: US-10-726-967a-84

Perfect score: 2288
Sequence: 1 TGGTGTPLRSLGAGAPLGL.....FVTLMDGCGINIPQTDST 433

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q/cgn2_1/usfto_spool_p/US10726967/runat 19082005 201241 29654/app query.fasta_1.583
-Db=Issued_Patents_NA -OPMT=fastap -SUPRT=nni -MINMATCH=0.1 -LOOPT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPM=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10726967 @CGN 1.1 105 @runat 19082005 201241 29654 -NCPU=6 -ICPU=3
-NO MAP -LAGGOUTERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAPN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/1/ina/5A COMB.seq: *
2: /cgn2_6/prodata/1/ina/5B COMB.seq: *
3: /cgn2_6/prodata/1/ina/6A COMB.seq: *
4: /cgn2_6/prodata/1/ina/6B COMB.seq: *
5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2267	99.1	1503	4	US-09-724-566A-1
2	2267	99.1	1503	4	US-09-471-669A-1
3	2267	99.1	2070	3	US-09-548-372D-3
4	2267	99.1	2070	3	US-09-548-372D-3
5	2267	99.1	2070	3	US-09-548-372D-3
6	2267	99.1	2070	4	US-09-351-853D-3
7	2267	99.1	2070	4	US-09-416-901B-3
8	2267	99.1	2070	4	US-09-548-372D-3
9	2267	99.1	2070	4	US-09-794-927A-3
10	2267	99.1	2070	4	US-09-548-372D-3
11	2267	99.1	2070	4	US-09-795-847B-3
12	2267	99.1	2070	4	US-09-548-366F-3

13	2267	99.1	2070	4	US-09-794-925A-3	Sequence 3, Appl1
14	2267	99.1	2070	4	US-09-806-194A-3	Sequence 3, Appl1
15	2267	99.1	2348	4	US-09-724-566A-42	Sequence 42, Appl1
16	2267	99.1	2348	4	US-09-724-566A-44	Sequence 44, Appl1
17	2267	99.1	2348	4	US-09-471-669A-42	Sequence 42, Appl1
18	2267	99.1	2348	4	US-09-471-669A-44	Sequence 44, Appl1
19	2267	99.1	3252	4	US-09-604-608-1	Sequence 1, Appl1
20	2267	99.1	5825	4	US-09-949-016-4382	Sequence 4382, Ap
21	2267	99.1	5878	4	US-09-949-016-939	Sequence 939, Ap
22	2267	99.1	16080	4	US-09-724-566A-48	Sequence 48, Appl1
23	2267	99.1	16080	4	US-09-471-669A-48	Sequence 48, Appl1
24	2267	99.1	2070	4	US-09-863-414-3	Sequence 3, Appl1
25	2261	98.8	2541	3	US-09-009-191-1	Sequence 1, Appl1
26	2257	98.6	1302	3	US-09-548-372D-25	Sequence 25, Appl1
27	2257	98.6	1302	3	US-09-548-372D-25	Sequence 25, Appl1
28	2257	98.6	1302	3	US-09-551-853D-25	Sequence 25, Appl1
29	2257	98.6	1302	4	US-09-416-901B-25	Sequence 25, Appl1
30	2257	98.6	1302	4	US-09-548-376D-25	Sequence 25, Appl1
31	2257	98.6	1302	4	US-09-794-927A-25	Sequence 25, Appl1
32	2257	98.6	1302	4	US-09-548-373D-25	Sequence 25, Appl1
33	2257	98.6	1302	4	US-09-795-847B-25	Sequence 25, Appl1
34	2257	98.6	1302	4	US-09-863-414-25	Sequence 25, Appl1
35	2257	98.6	1302	4	US-09-548-366F-25	Sequence 25, Appl1
36	2257	98.6	1302	4	US-09-548-368D-25	Sequence 25, Appl1
37	2257	98.6	1302	4	US-09-794-925A-25	Sequence 25, Appl1
38	2257	98.6	1302	4	US-09-806-194A-25	Sequence 25, Appl1
39	2257	98.6	1341	3	US-09-548-372D-21	Sequence 21, Appl1
40	2257	98.6	1341	3	US-09-548-367D-21	Sequence 21, Appl1
41	2257	98.6	1341	4	US-09-551-853D-21	Sequence 21, Appl1
42	2257	98.6	1341	4	US-09-416-901B-21	Sequence 21, Appl1
43	2257	98.6	1341	4	US-09-548-376D-21	Sequence 21, Appl1
44	2257	98.6	1341	4	US-09-794-927A-21	Sequence 21, Appl1
45	2257	98.6	1341	4	US-09-548-373D-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-09-724-566A-1
Sequence 1, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Gurigbal
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Srinha, Sukanto
APPLICANT: Tateuno, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
TITLE OF INVENTION: Methods
FILE REFERENCE: 228-US-NWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-566A-1

Alignment Scores:

Pred. No.: 2,59e-257 Length: 1503
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 4 Gaps: 0
 US-10-726-967a-84 (1-433) x US-09-724-566a-1 (1-1503)

QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
 DB 64 ACCGACGACGGCATCGGCTGCGCGACGGGCTGGGGGGCGCCCCCTGGGGCTG 123
 QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyArgGlySerPheVal 40
 DB 124 CGGCTGCCCCGGGAGACCGACGAGAGCCCGAGGCCCGGAGGGGAGCTTTGGT 183
 QY 41 GluMetValAspAsnLeuArgGlyLeuSerGlyGlnGlyTyrValGluMetThrVal 60
 DB 184 GAGATGGTGGACAACTGAGGGGCAAGTCGGGGCAGGGCTTACGTCGAGATGACCGTG 243
 QY 61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
 DB 244 GGCAGCCCCCGGACGACCTTACACATCTGCTGGATACAGGCGACGCTCCACACATAC 303
 QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
 DB 304 GGTCTGCCCCCGACCCCTCTCTCATCTGCTACTACAGGAGGAGGCTCCACACATAC 363
 QY 101 ArgAsnLeuArgGlyValTyrValProTyrThrGlnGlySerTyrGluGlyLeu 120
 DB 364 CGGACCTCCGAGAGGGTGTATGTCCTCTACACCCAGGGCAAGTGGGAGGGAGCTG 423
 QY 121 GlyThrAsnLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
 DB 424 GGCACCGACCTGGTACATCCCCACGCCCCCACTGCTGCTGCCAATGCT 483
 QY 141 AlaIleThrGlnSerAspArgPhePheIleAsnGlySerAsnTyrGluGlyLeuGly 160
 DB 484 GGCATCATGAAATGACGAAAGTTCTTCACTACACGCTCCAACTGGGAGGAGATCCCTG 543
 QY 161 LeuAlaTyrAlaGluIleAlaTyrProAspAspSerLeuGluProPheAspSerLeu 180
 DB 544 CTGGCTGATGCTAGATTCGACAGCTGACGACTCCCTGAGCCCTTCTTATCTCTTG 603
 QY 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuCysGlyAlaGlyPhePro 200
 DB 604 GTAAACCAACCCACCTCTCCAACTCTCTGACAGCTTGTGGTGGCTGCCCTCC 663
 QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlySerMetIleGlyGlyIleAsp 220
 DB 664 CTCAACCATCTGAAGTCTGCTGCTGCGAGGAGCATGATATTTGGAGATTCAC 723
 QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
 DB 724 CACTGCTGTACACAGGAGCTCTGTGTATACACCACTCCGGCGGAGTGTATTATGAG 783
 QY 241 ValIleIleValArgValGluIleAsnGlyIleAsnLeuGlyMetAspCysLeuGlyTyr 260
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 QY 261 AsnTyrAspLeuSerIleValAspSerGlyThrThrAsnLeuArgLeuProValVal 280
 DB 844 AACCTATGACAGAGCATTTGTGGACGTGGACACCAACCTTCTTTGCCCCAAGAAAGTG 903
 QY 281 PheGluAlaAlaValIleSerIleLeuAlaAspSerThrGluTyrPheProAspGly 300
 DB 904 TTGAAAGTGCAGTCAATCATCAAGGACGCTCTCCACGAGAGAGTTCCCTGATGCT 963
 QY 301 PheTyrLeuGlyGluGlnLeuValCysTyrGlnIleGlyThrThrProTyrPheIlePhe 320
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QY 321 ProValIleSerLeuTyrLeuMetGlyValValThrAsnGlnSerPheArgIleThrIle 340
 DB 1024 CCAAGTATCTTCACTTACCTTAATGGGTAGGTACCAACAGTCTTCCGATACCATC 1083
 QY 341 LeuProGlnGluTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
 DB 1084 CTTCCGCGACATATCTCGCGCAGTGGAGATGGGCAAGTCCCAAGAGACTTTAC 1143
 QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGly 380
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 QY 401 ValHisAspGluPheAsnGluThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
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 DB 1324 GACTGTGGCTTACATTCATTCACAGACAGATGATCAACC 1362

RESULT 2
 US-09-471-669A-1
 / Sequence 1, Application US/09471669A
 / Patent No. 6830918
 / GENERAL INFORMATION:
 / APPLICANT: Anderson, John P.
 / APPLICANT: Basi, Guribhai
 / APPLICANT: Doane, Minh Tam
 / APPLICANT: Frigon, No. 6830918mand
 / APPLICANT: John, Varghese
 / APPLICANT: Power, Michael
 / APPLICANT: Sinha, Sukanto
 / APPLICANT: Tatsuno, Gwen
 / APPLICANT: Tung, Jay
 / APPLICANT: Wang, Shuwen
 / APPLICANT: McConlogue, Lisa
 / APPLICANT: Elian Pharmaceuticals, Inc.
 / TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
 / FILE REFERENCE: 015270-006430US
 / CURRENT APPLICATION NUMBER: US/09/471, 669A
 / CURRENT FILING DATE: 1999-12-24
 / PRIOR FILING DATE: 1998-12-31
 / PRIOR APPLICATION NUMBER: US 60/114, 408
 / PRIOR FILING DATE: 1999-02-10
 / PRIOR APPLICATION NUMBER: US 60/139, 172
 / PRIOR FILING DATE: 1999-06-15
 / NUMBER OF SEQ ID NOS: 108
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 1
 / LENGTH: 1503
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-09-471-669A-1

Alignment Scores:
 Pred. No.: 2,59e-257 Length: 1503
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 4 Gaps: 0

US-10-726-967a-84 (1-433) x US-09-471-669a-1 (1-1503)
 QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
 DB 64 ACCGACGACGGCATCGGCTGCGCGACGGGCTGGGGGGCGCCCCCTGGGGCTG 123

QY	21	GIuIlleAmLeGluThraApGluGluProGluGluProGlyAraGrGlySerPheVal	40
DB	124	CGGCTGCCCGGAGACCGACGAAAGGCCCGAGAACCCGGCCGGAGGGGCAAGCTTTGG	183
QY	41	GIuMeTValAaRApNuLeuAraGlyLyvSesrGlyngInGlyTyrTyrValGIuMeTThVal	60
DB	184	GAGATGGTGAACAACCTGAGGGGCAAGTCGGGGCAGGGCTTACTGATGATGACCGTG	243
QY	61	GIySerProGlnThrLeuAsnIleLeuValAspThrGIySerSerAsnPheAlaVal	80
DB	244	GCGACGCCCCCGCAGACGCTCAACACCTCGTGGATGACGAGCAGTAACTTGGACGTG	303
QY	81	GIyAlaAlaProHisProPheLeuHisArgTyrTyrGlnAraGlnLeuSerSerThrTyr	100
DB	304	GGTGCTGCCCCCAACCCCTTCCTGCATCGCTACTACAGAGGCAAGCTGTCCAGCAATAC	363
QY	101	ArgAraPheAraGlyLyvGlyValTyrValProTyrThrGlnGlyLyvTrrpGluGlyLeuLeu	120
DB	364	CGGAGACTCCGGAGGGGTGTGTATGTGCCCTTACACCGAGGCAAGTGGAGGGAGAGCTG	423
QY	121	GIyTrpAspLeuValSerIleProHisGlyProAsnValThrValAraGlnAaenIleAla	140
DB	424	GCGACCGACCTGGTGAAGCATCCCCCATGGCCCAAGTCACTGTGGTGCACATTTGGT	483
QY	141	AlaIleThrGluSerAspLyvPhePheIleAmGlySerAsnTrpGluGlyIleLeuGly	160
DB	484	GGCATCACTGAATCAGACAAAGTTCTTCATCAAGGCTCCAACTGGAGAGGCATCTCGGG	543
QY	161	LeuAlaTyrAlaGluIleAlaArgProAraAspSerLeuGluProPhePheAspSerLeu	180
DB	544	CTGGCCTTAAGCTGAAGATTGCCAGGCGTGAAGCATCTCGTAGGCTTTCTTGACTCTG	603
QY	181	ValLyvGlnThrHisValProAsnLeuPheSerLeuGlnLeuCySGlyAlaGlyPhePro	200
DB	604	GTAAGCAAGCCCACTTCCCAACTCTTCTCCCTGCAAGTTGTGGTGTGGCTTCCC	663
QY	201	LeuAmGlnSerGluValLeuAlaSerValGlyLyvSerMetIleIleGlyGlyIleAsp	220
DB	664	CTCAACCAAGCTGAAGTGGCTGCTCTGTGGAGGAGCATGTATCATTTGAGGATATCGAC	723
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QY	261	AsnTyrAspLyvSerIleValAspSerGlyThrThrAsnLeuArgLeuProLyvLyvVal	280
DB	844	AACATAGACAAGACATTTGTGGACAGTGGCACCAACCACTTGCTTGCCCAAGAAAGTG	903
QY	281	PheGlnAlaAlaValLyvSerIleLyvAlaAlaSerSerThrGluLyvPheProAsnGly	300
DB	904	TTTGAAGCTGCAATCAATCATCAAGGACGCTCTCCACGAGAAAGTTCCCTGAAGGT	963
QY	301	PheTrpLeuGlyGlyGlnLeuValCysTrrpGlnAlaGlyThrThrProTrrpAsnIlePhe	320
DB	964	TTTGGCTGAAGAGACAGCTGTGTGTGTGGCAAGCAGGACACACCTTGGAACTTTTC	1020
QY	321	ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle	340
DB	1024	CCAGTCATCTCACTTCACTTAATGGGAGAGTTCACCAACAGTCTTCCGATCAACATC	1083
QY	341	LeuProGlnGlnTyrIleLeuArgProValGluAspValAlaHisSerGlnAraAspCySer	360
DB	1084	CTTCCGAGCAAAATACCTGGCGCCACGTGAAGATGTGGCCACGTCCTCAAGACGATGTTAC	1143
QY	361	LyvPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly	380
DB	1144	AAGTTTGCCATCTCAACGTATCCACGGGCACTTTATGGGAAGCTGTATTATCATGAAGGC	1203
QY	381	PheTyrValValPheAspArgAlaArgLyvArgTlleGlyPheAlaValSerAlaCyHis	400

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Qy	421 AERCYRGLYTYTAAsn1LeProGlnThraAspGlySerThr	433					
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; Patent No. 6420534							
; GENERAL INFORMATION:							
; APPLICANT: GURNEY ET AL.							
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES							
; FILE OF INVENTION: THEREOF							
; FILE REFERENCE: 29915/62801							
; CURRENT APPLICATION NUMBER: US/09/548, 372D							
; CURRENT FILING DATE: 2000-04-12							
; PRIOR APPLICATION NUMBER: US 60/155,493							
; PRIOR FILING DATE: 1999-09-23							
; PRIOR APPLICATION NUMBER: US 09/404,133							
; PRIOR FILING DATE: 1999-09-23							
; PRIOR APPLICATION NUMBER: PCT/US99/20881							
; PRIOR FILING DATE: 1999-09-23							
; PRIOR APPLICATION NUMBER: US 60/101,594							
; PRIOR FILING DATE: 1998-09-24							
; NUMBER OF SEQ ID NOS: 73							
; SOFTWARE: PatentIn version 3.1							
; SEQ ID NO 3							
; LENGTH: 2070							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
US-09-548-372D-3							
Alignment Scores:							
Pred. No.: 4,34e-257 Length: 2070							
Score: 2267.00 Matches: 429							
Percent Similarity: 99.31% Conservative: 1							
Beet Local Similarity: 99.08% Mismatches: 3							
Query Match: 99.08% Indels: 0							
DB: 3 Gaps: 0							
US-10-726-967A-84 (1-433) x US-09-548-372D-3 (1-2070)							
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Db	124 CGGCTCGCCCGGAGACCGACGAGAGCGCCGAGAGCGCCGCGGCGGAGCGCTTGTG	183					
Qy	41 G1uMeVal1AspAsnLeuArgG1YLYSerG1YGL1YTYTYVal1G1uMeThrVal	60					
Db	184 GAGATGTGGACAACTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGGAGATGACCGTG	243					
Qy	61 G1YSerProProGlnThraAsn1LeuVal1AspThrg1YSerSerAsnPhe1aVal	80					
Db	244 GGAAGCGCCCGGAGAGCGCTCAACATCTCTGTGATGACACGACAGATGACTTTCAGTG	303					
Qy	81 G1YAlAlAProH1sProPheLeuH1sArgTYTYTYG1nArgG1nLeuSerSerThrTYr	100					
Db	304 GGGCTGCCCCCAACCTTCTCTGATCGTACGACAGGACGCTGTCCAGACATAC	363					
Qy	101 ArgAspLeuArgLYSerG1YVal1ProTYThrg1nG1YLYTYPrG1uG1YGL1uLeu	120					
Db	364 CGGACCTCGGAGAGGCTGTGTATGTGCCCTTACACCCAGGCGCAAGTGGAGGGGAGCTG	423					
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Db 484 GGCATCAGCAATGACAGCAAGTCTTCATCAACGGCTCCAACTGGGAAGGATCCTGGG 543
Qy 161 LeuAlaTrpAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
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Qy 181 ValIyGlnThrHisValProAsnLeuPheSerLeuGlnLeuCyGlyAlaGlyPhePro 200
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Qy 201 LeuAengIySerGlnValLeuAlaSerValGlyIySerMetIleIleGlyIyIleAsp 220
Db 664 CTCAACCAAGTCTGAAGTCTGAGCTGTGTGAGAGAGGAGCATGATTCATGGAGGTATCGAC 723
Qy 221 HisSerLeuTyTrpGlySerLeuTrpTyTrpProIleArgAspGluTrpTyTrpGlu 240
Db 724 CACTGCTGTACACAGGCAAGTCTGTGATACCCATCCGCGGAGTGTATATAG 783
Qy 241 ValIleIleValIaArgValGluIleAengIyGlnAspLeuLysMetAspCyGlyGlyIy 260
Db 784 GTCAATCATTTGCGAGTGAATGATGATGACAGAGATCTGAATAATGACCTGCAAGAGATAC 843
Qy 261 AsnTyAspLysSerIleValAspSerGlyTrpThrAsnLeuArgLeuProLysVal 280
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RESULT 4
US-09-548-367D-3
; Sequence 3, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280H
; CURRENT APPLICATION NUMBER: US/09/548,367D
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; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-367D-3

Alignment Scores:
Pred. No.: 4,34e-257 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 3 Gaps: 0

US-10-726-967a-84 (1-433) x US-09-548-367D-3 (1-2070)

Qy 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyIleuGlyValIaProLeuGluIleu 20
Db 64 ACCAGACAGCGGCATCGGCTGCGCCCTGCGAGAGGCTTGGGGGCGCCCTTGAGGGCTG 123
Qy 21 GluIleAsnLeuGluTrpAspGluGluProGluGluProGlyIaArgArgIySerPheVal 40
Db 124 CCGGTGCCCCGGAGAGCCGAGAGAGCCGAGAGCCCGCGAGCGGCGAGGCGAGCTTGTG 183
Qy 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTrpTyTrpValGluMetThrVal 60
Db 184 GAGATGTGTGACAACTGAGAGGCGCAAGTGGGGAGAGGCTTACGTGAGATGACCGTG 243
Qy 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 244 GGCAGCCCCCGGAGAGGCTCAACATCTGTGTGATACAGCAGCAGTAACTTTCAGTG 303
Qy 81 GlyAlaIleProHisProPheLeuHisArgTyTrpGlnArgGlnLeuSerSerThrTyTr 100
Db 304 GGTGTGCCCCCAACCCCTTCTGCATCGCTACCTACAGAGGAGCACTGTCCAGCATATC 363
Qy 101 ArgAspLeuArgLysGlyValIyTrpValProTyTrpGlnGlyLysTrpGluGlyIleu 120
Db 364 CCGGACCTCCGGAAGGAGTGTATGTGCCCTACACCGAGGCGAAGTGGGAAGGAGCTG 423
Qy 122 GlyThrAspLeuValSerIleProHisGlyProAsnValIleThrValArgAlaAsnIleAla 140
Db 424 GGACCGGACCTGTAAAGATCCCATGAGCCCAACGTCATGTGCGTGCACAACTTGTCT 483
Qy 141 AAlIeThrGluSerAspLysPhePheIleAengIySerAsnTrpGluGlyIleuGly 160
Db 484 GGCATCAGCAATGACAGCAAGTCTTCATCAACGGCTCCAACTGGGAAGGATCCTGGG 543
Qy 161 LeuAlaTrpAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCTTAAGTGAATTCAGATTCAGGAGCTTGAAGCACTCCGAGAGCTTCCTTGAAGCTCTG 603
Qy 181 ValIyGlnThrHisValProAsnLeuPheSerLeuGlnLeuCyGlyAlaGlyPhePro 200
Db 604 GTAAAGCAGAGACCAAGTCCCAACTCTTCCCTCCGAGAGCTTGGTGGCTGGCTTCCC 663
Qy 201 LeuAengIySerGlnValLeuAlaSerValGlyIySerMetIleIleGlyIyIleAsp 220
Db 664 CTCAACCAAGTCTGAAGTCTGAGCTGTGTGAGAGAGGAGCATGATTCGAGATTCGAC 723
Qy 221 HisSerLeuTyTrpGlySerLeuTrpTyTrpProIleArgArgGluTrpTyTrpGlu 240
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Db 724 CACTGCTTACACAGGCACTCTCTGTATACACCATCCGGGAGTGTATTATGAG 783
Qy 241 VALLIIEIIEVALARGVALGIUIIEANGIYGINAPLEULYMEASPPCYALYSGLIYR 260
Db 784 GTCAATCATTTGTCGGGTGAGATCAATGACAGGATCTGAATAATGACATGCAAGGATAC 843
Qy 261 AANTYRASPYSERIEVALASPSENGIYTHRTTHANLEUARGLEUPROLYSIVSVAL 280
Db 844 AACCTATGACAAAGCAATTTGTGACATGACACCAACCTTGTGTCCTTCCCAAGAAAGTG 903
Qy 281 PHEGUALAALAVALLYSERIELEYSALIASERSETHGJULYSPHEPROAPGY 300
Db 904 TTTGAAGCTGCACTCAATCCATCAAGGACCTCTTCCAGAGAAAGTTCCCTATGCT 963
Qy 301 PHETRPLEUGLYGLUGLNULEUVALCYSTRPGINAGIYTHRTTHPROTRPANIIEPHE 320
Db 964 TTCTGGCTAGAGAGACAGCTGGGTGCTGGCAAGCAGGACCACTTGGAAACATTTTC 1023
Qy 321 PROVALIIESELEUYTRIEUWETGLYGLUVALIETHANGINSEPHETRGIIETHRIE 340
Db 1024 CCAAGTCATCTCACTTAACCTAATGGGTGAGTTAACCAACCACTCTTCCGACATCACCATC 1083
Qy 341 LEUPROGLINGIYTRIEUARGPROVALGIUASPVALLATHSERGINASPPASPPCYSTR 360
Db 1084 CTTCGCAACATACCTTGGGCGGCGAGTGAAGATGTGGCCACCTCCAAAGCACTGTAC 1143
Qy 361 LYSPEHALIIESEGINSESETHRGITHTHVALMETGLIALAVALLIEMETGLIY 380
Db 1144 AGTTTGCATCTCAAGTCATCAAGGACAGCTGTTATGGAGCTGTATACATGAGAGGC 1203
Qy 381 PHEYTRVALIAPHEAPARGALAAAGLYEARGILEGLYPHEALIAVASERLACYSHIS 400
Db 1204 TTCTAGTTGTCTTTCATCGGGGCCGAAAAAGAAATGGCTTGTCTGACCGCTTGCCAT 1263
Qy 401 VALHIAASPGIUPHEARTRTHALIAVALIGLUGIYPROPHETVALIETHLEUASPPMETGLI 420
Db 1264 GTGCAAGATGAGTTGACAGAGCGGAGCGGTGGAGGCCCTTTTGTCACTTGGACATGAA 1323
Qy 421 AASPCEGLIYTRASNIIEPROGINTHRASPGLUSETHR 433
Db 1324 GACTGTGGCTACAACTTCACAGACAGATGATCAACC 1362
RESULT 5
US-09-551-853D-3
; Sequence 3, Application US/09551853D
; Patent No. 6500667
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280L
; CURRENT APPLICATION NUMBER: US/09/551,853D
; CURRENT FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-551-853D-3
Alignment Scores:
Pred. No.: 4,34e-257 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1

Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 4 Gaps: 0
US-10-726-967A-84 (1-433) x US-09-551-853D-3 (1-2070)
Qy 1 THRGINISGLIIEARGLEUPROLEUARGSERGLYLEUGIYGLIALAPROLEUGIYLEU 20
Db 64 ACCAGCAAGGATCTGGCTGCCCTGGCAGCGGCTGGGGGGGGCCCTGGGGGCTG 123
Qy 21 GIUIEAMLEUGIUTHRASPGLUGIUPROGIYARGARGIYSEPHETVAL 40
Db 124 CGGCTGCCCGGAGAACCGAGAGAGCCCGAGAGAGCCCGGAGGAGGAGCTTTGTG 183
Qy 41 GIUWETVALASPPASPPASPPASPPASPPASPPASPPASPPASPPASPPASPPASPP 60
Db 184 GAGATGAGTGAACCACTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 243
Qy 61 GLYSERPROGINTHRTHEUANILEUVALASPTHRGLYSERASPPHEALIAVAL 80
Db 244 GGCACCCCGGAGACAGCTCAACATCTGTGATGATACAGGACAGATACCTTGCAGTG 303
Qy 81 GLIALAIAPROHIAASPPHEUHIASPTHTYTRGINAARGINLEUASPPASPPASPP 100
Db 304 GGTGCTGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 363
Qy 101 ARGASPPASPPASPPASPPASPPASPPASPPASPPASPPASPPASPPASPPASPP 120
Db 364 CGGAGCTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
Qy 122 GIYTHRASPHEUVALSERIEPROHISGLIYPROASPVALLATHVALARGALASNIIEAL 140
Db 424 GGCACCGACCTGTGTAAGCATCCCAAGGCCCAAGCTGATGCTGCTGCTGCTGCTGCTGCT 483
Qy 141 ALAIETHRGUSEASPPASPPHEHIEANGIYSEASPTHTGUGIYIIELEUGIY 160
Db 484 GGCATCATGATGACAGCAAGATTTTCATCAACGAGCTCCAACTGGAGAGGACCTCTGGGG 543
Qy 161 LEUALATYRAGIUIIEALARGPROASPPASPPASPPASPPASPPASPPASPPASPP 180
Db 544 CTGGCTATGCTGAATTCGCGAGGCTGACGACTCCCTGGAGCCTTTTCTTAACCTCTG 603
Qy 181 VALIVSGINTHRTHEIALPROHISLEUASPPHESELEUGINLEUCYGLIALAGIYPHEPRO 200
Db 604 GTAAAGCAAGACCAAGTTCCCAACTCTTCTCCCTGACCTTTGGGTGCTGCTGCTGCTGCT 663
Qy 201 LEUANGINSEGLIUALLEUALASERYALGIYSEMEIEIEGLIYIIEAP 220
Db 664 CTCAACAGCTCGAAGTGTGCTCTGTGCGAGGAGATGATCATTTGAGAGGTATCGAC 723
Qy 221 HISERLEUYTRTHGLYSERLEUTPTHTHPTROIEARGARGIUTPTHTYTRGIU 240
Db 724 CACTGCTGTACACAGGAGTCTCTGTATACACCACTCCGGGAGGAGGTATTATGAG 783
Qy 241 VALLIIEIIEVALARGVALGIUIIEANGIYGINAPLEULYMEASPPCYALYSGLIYR 260
Db 784 GTCAATCATTTGTCGGGTGAGATCAATGACAGGATCTGAATAATGACATGCAAGGATAC 843
Qy 261 AANTYRASPYSERIEVALASPSENGIYTHRTTHANLEUARGLEUPROLYSIVSVAL 280
Db 844 AACCTATGACAAAGCAATTTGTGACATGACACCAACCTTGTGTCCTTCCCAAGAAAGTG 903
Qy 281 PHEGUALAALAVALLYSERIELEYSALIASERSETHGJULYSPHEPROAPGY 300
Db 904 TTTGAAGCTGCACTCAATCCATCAAGGACCTCTTCCAGAGAAAGTTCCCTATGCT 963
Qy 301 PHETRPLEUGLYGLUGLNULEUVALCYSTRPGINAGIYTHRTTHPROTRPANIIEPHE 320
Db 964 TTCTGGCTAGAGAGACAGCTGGGTGCTGGCAAGCAGGACCACTTGGAAACATTTTC 1023
Qy 321 PROVALIIESELEUYTRIEUWETGLYGLUVALIETHANGINSEPHETRGIIETHRIE 340
Db 1024 CCAAGTCATCTCACTTAACCTAATGGGTGAGTTAACCAACCACTCTTCCGACATCACCATC 1083

QY 341 LeuProGlnGlnTyrLeuAspProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1084 CTTCCGAGCAATATCTGGCGGAGAGATGTGGCCACGTCACCAAGACGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGluValIleMetGluGly 380
Db 1144 AGTTTGGCATCTCAAGTCATCCACGGGCACTGTTATGGAGCTGTATCATGAGGGC 1203
QY 381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1204 TTCTAGTGTCTGTGATCGGGCCCGAAACGAATTGGCTTGTCTGTCAAGCGCTTGGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGACAGATGATTCACAGACGGACCGGTGAAGGCCCTTGTCTACCTTGGACATGGAA 1323
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTACACATTCACAGACGATGATCAACC 1362

RESULT 6

US-09-416-901B-3
; Sequence 3, Application US/09416901B
; Patent No. 6639671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280A
; CURRENT APPLICATION NUMBER: US/09/416,901B
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20861
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-416-901B-3

Alignment Scores:

Pred. No.: 4,34e-257 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 4 Gaps: 0

US-10-726-967A-84 (1-433) x US-09-416-901B-3 (1-2070)

QY 1 ThrGlnHisGlyIleAspGluProLeuArgSerGlyLeuGlyGlyValAlaProLeuGlyLeu 20
Db 64 ACCCGACAGGAGCTCGGCTGCCCTGGCGACGGGCTGGGGGGGCGCCCTCGGGGCTG 123
QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyLysArgGlySerPheVal 40
Db 124 CGGCTGCCCGGAGACCGAGAAAGCCCGAGAGCCCGCGAGGGGAGGCTTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
Db 184 GAGAGTGGTGAACAACTGAGGGGCAAGTCGGGGGCAAGGCTACCTACGTGAGATGACCGTG 243
QY 61 GlySerProGlnThrLeuAsnIleValAspThrGlySerSerAsnPheAlaVal 80
Db 244 GGCAGCCCCCGGACGCTCAATCTGTGTGATACAGGACAGACTAACTTTGACGTG 303

QY 81 GlyValAlaProHisProPheLeuHisArgTyrTyrGlnAspGlnLeuSerSerThrTyr 100
Db 304 GGTGCTGCCCCCACCCTCTCTGTCATGCACTACCGAGAGGAGCTGTCCAGACATAC 363
QY 101 ArgAspLeuArgLysGlyValTyrValProTyrThrGlnGlyLysTPGlnGlyLeu 120
Db 364 CGGAGCTCCGGAAGGGTGTATGTGCTTCACCCAGGACAAAGTGGAAAGGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 424 GGCACCGACTGTGTAGCATCCCATGCGCCCAACGTCACGTGGCTGCCAACATTTGCT 483
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnLysSerAsnTPGlnGlyIleLeuGly 160
Db 484 GCCATCATGAAATGACAAAGTTTTCATCAACGGCTCAACTGGGAAAGCATCTGGGG 543
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCTATGTGTGAGATTGCAAGGCTGACGACTGCCCTGAGGCTTTCTTGTACTCTTG 603
QY 181 ValLysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCysGlyAlaGlyPhePro 200
Db 604 GTAAAGCAACCCACGTTCCCACTCTTCTCCCTGACGCTTGTGTGTGCTGCTTCCCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyLysMetIleIleGlyGlyIleAsp 220
Db 664 CTCAACGACTGTGAAGTGTGGCTCTGTGTGAGGAGATATCATTTGAGGTATCGAC 723
QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
Db 724 CACTCGCTGTACAGGACAGTCTGTGTATACACCATCCGCGGAGGTGATATATGAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLysGlyTyr 260
Db 784 GTCATCATTTGTGGGGGTGAGATCATGACAGGATCTAAATGTGACTGCAAGGAGTAC 843
QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 844 AACTATGACAAAGCAATGTGTGACATGTGCACACCAACTTCGTTGCCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValLysSerIleLysAlaIleSerSerThrGluLysPheProAspGly 300
Db 904 TTGAAGCTGAGTCAATCATTCATCAAGGAGCTCTTCCAGGAAAGTTCCCTGATGT 963
QY 301 PheTyrLeuGlyGluGlnLeuValCysTyrGlnAlaGlyThrThrProTyrAsnIlePhe 320
Db 964 TTCTGGCTAGAGAGAGAGCTGTGTGTGTCGCAAGGACACCACTTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAAGTATCTCACTTCAATATGGGTAGGTATCAACCAAGCTCTTCCGATCAACATC 1083
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1084 CTTCCGACGCAATATCTCGGCGAGTGAAGATGTGGCAAGTCCCAAGACGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1144 AGTTTGGCATCTCAAGTCATCCACGGGCACTGTATGGAGCTGTATCATGAGGGC 1203
QY 381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1204 TTCTAGTGTCTGTGATCGGGCCCGAAACGAATTGGCTTGTCTGTCAAGCGCTTGGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGACAGATGATTCACAGACGGACCGGTGAAGGCCCTTGTCTACCTTGGACATGGAA 1323
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTACACATTCACAGACGATGATCAACC 1362

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RESULT 7
US-09-548-376D-3
; Sequence 3, Application US/09548376D
; Patent No. 6706485
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR
; TITLE OF INVENTION: AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-548-376D-3

Alignment Scores:
Pred. No.: 4,34e-257 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0

US-10-726-967A-84 (1-433) x US-09-548-376D-3 (1-2070)
QY 1 ThrGlnHieGlyIleArgLeuProLeuArgSerGlyLeuGlyValIleProLeuGlyLeu 20
DB 64 ACCCAACACCGGATCCGGCTGGCCCTGGCGAGCGGCTGGGGGCCCCCTGGGGCTG 123
QY 21 GluIleAsnLeuGluThrArgGluProGluGluProGlyArgArgGlySerPheVal 40
DB 124 CGGCTCCCGGGGAGACCGGACGAAGCCCGGAGAGCCCGGCGAGGGCCACTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
DB 184 GAGATGCTGACAACTGAGAGGCGCAAGTCGGGCGAGGCTACTACGTGAGATGACCGTG 243
QY 61 GlySerProGluInThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
DB 244 GGGAGCCCCCGGAGAGCTCAACATCTGTGTGATACAGGCACTTGTGACGTG 303
QY 81 GlyAlaIleAspProIleAspPheLeuHieArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
DB 304 GGTCGTGCCCCCAACCCCTTCTGCACTGCTACTACACAGGAGGCTGTCCACACATAC 363
QY 101 ArgAspLeuArgGlyValIleTyrValProTyrThrGlnGlyLysTyrGluGluLeu 120
DB 364 CGGAGCTTCGGAGAGGTGTGTATGTGCTCTACACCCAGGGCAAGTGGAGAGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHieGlyProAsnValThrValArgAlaAsnIleAla 140
DB 424 GGGACGCACTGTGTAAGCATCCCCCACTGAGCCCACTCACTGTGCTGTGCAACATTC 483
QY 141 AlaIleThrGlySerAspLysPhePheIleAsnGlySerAsnTyrGluGlyIleLeuGly 160
DB 484 GGCATCACTGAATCAGCAAGTCTTCTCATCAAGGCTCCAACTGGGAGGACATCTCTGG 543
QY 161 LeuAlaTyrTrpIleGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180
DB 544 CTGGCTATGCTGAGATTGCAAGGCTGAGCACTCCCTGGAGCCTTCTTGTGACTCTG 603

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QY 161 ValIleGlyInThrHieValProAsnLeuPheSerLeuGlnLeuCyGlyValIleGlyPhePro 200
DB 604 GTTAAAGCAGACCCAGGATCCCAACTCTTCTCCCTGACAGCTTGTGTGCTGCTCC 663
QY 201 LeuAsnGlnSerGluValIleuAlaSerValGlyIleSerMetIleIleGlyIleAsp 220
DB 664 CTCAACCACTGTAAGTGTCTGCTCTGTGGAGGAGCATGATCATTTGAGATTCGAC 723
QY 221 HisSerLeuTyrThrGlySerLeuTyrThrProIleArgArgGluTyrTyrGlu 240
DB 724 CACTGCTGTACACAGGAGCTCTGTGTATACCCATCCGCGGAGGTGGATATATAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCyGlySerGly 260
DB 784 GTCATCATTTGGCGGGTGGAGTCAATGACAGATCTGAAATGACTGACAGAGTTC 843
QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
DB 844 AACTATGACAGAGCATTTGTGACAGTGGACACCAACCTTCTGTGGCCAAAGTGG 903
QY 281 PheGluAlaIleValIleSerIleLysAlaIleSerThrGluLysPheProAspGly 300
DB 904 TTTGAAGCTGACGTCAAATCCATCAAGCAGCTCTCTCCACGAGAAATTCCTGATGT 963
QY 301 PheTyrPheGlyGluGluLeuValCysTyrGlnIleArgIleThrThrProTyrAsnIlePhe 320
DB 964 TTCTGTGCTAGGAGACAGCTGTGTGTGCTGGCAAGGACCAACCCCTTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB 1024 CAGTCATCTCACTCACTACTATATGGGTAGATTCACCAACCACTCTCCGATCAACATC 1083
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
DB 1084 CTTCCGAGCAATACCTGGCGCCAGTGGAAATGTGCCCACCTCCCAACACACACTGTTC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyTyrThrValMetGlyAlaValIleMetGluGly 380
DB 1144 AAGTTTGCATCTCAACAGTATCAAGGCACTGTATAGGAGCTGTATCATCGAGGAC 1203
QY 381 PheTyrValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
DB 1204 TTCTACGTTGTCTTGTATGCGGCCCGAAACAAATTTGCTTGTGCTGACGCGTGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1264 GTGACAGATGAGTTCAGACGCGCAGGCGTGAAGGCCCTTTGTCTCACTTGACATGAA 1323
QY 421 AspCyGlyTyrAsnIleProGlnThrAspGluSerThr 433
DB 1324 GACTGTGCTACAACTTCACAGACGATGAGTCAACC 1362

RESULT 8
US-09-794-927A-3
; Sequence 3, Application US/09794927A
; Patent No. 6727074
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594

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PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2070
TYPE: DNA
ORGANISM: Homo sapiens
US-09-794-927A-3

Alignment Scores:

Pred. No.:	4,34e-257	Length:	2070
Score:	2267.00	Matches:	429
Percent Similarity:	99.31%	Conservative:	3
Best Local Similarity:	99.08%	Mismatches:	1
Query Match:	99.08%	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-84 (1-433) x US-09-794-927A-3 (1-2070)

QY 1 ThrGlnHISGlyILEArgLeuProLeuArgSerGlyLeuGlyGlyValAlaProLeuGlyLeu 20
Db ACCACGACGCGCATCCGGCTCCCTCGGACAGCGGCTCGGGGGGCGCCCTCGGGGCTG 123
QY 21 GluILEanLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
Db CGGCTGCCCGGAGACCGACGAAAGAGCCCGAGGAGCCGGCCGGAGGGGCACTTTGTC 183
QY 41 GluMetValAspAanLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
Db GAGATGGTGACACCTGAGGGGCAAGTCGGGGCAAGGCTTACCTGAGATGACCGCTG 243
QY 61 GlySerProProGlnThrLeuAanILEuValAspThrGlySerSerAsnPheAlaVal 80
Db GGCAGCCCCCGGACGCTCAACATCTGTGGATACAGGACGATTAATTGACATG 303
QY 81 GlyAlaAlaProHisProPheLeuHISArgTyrTyrGlnArgGlnLeuSerThrTyr 100
Db GGTGGTCCCCCGACCTTCCTGACATCGCTACACAGGACGCTGTCAGACATAC 363
QY 101 ArgAspLeuArgLysGlyValTyrValProTyrThrGlnGlyLysTyrPheGluGlu 120
Db CGGACCTCCGGAAGGTGTGTATGTCCTTACACCCAGGACGAGTGGAGAGGAGCTG 423
QY 121 GlyThrAspLeuValSerILEProHISGlyProAsnValThrValArgAlaAsnILEa 140
Db GGCACGACCTGGTGAAGCATCCCGCATGGCCCCACGATCATGTGCTCCAACTTGT 483
QY 141 AlaILEThrGlySerAspLysPhePheILEanGlySerAsnTyrGlnGlyILEuGly 160
Db GGCATCATCGAATCAGACAAAGTTCTTCAACAGGCTCCACCTGGAGAGGCACTTGGGG 543
QY 161 LeuAlaTyrAlaGluILEaArgProAspAspSerILEuGluProPhePheAspSerLeu 180
Db CTGGCTATAGCTGAGATTCAGAGGCTGAGCTCCCTGAGGCTTTCTTTGACTCTCTG 603
QY 181 ValLysGlnThrHISValProLeuLeuPheSerILEuGlnLeuGlyValGlyPhePro 200
Db GTHAAGACACCCAGGTTCCAACTTCTCCGACGCTTGGGCTGGCTGGCTTCC 663
QY 201 LeuAnGlnSerGluValLeuAlaSerValGlyLysSerMetILEGlyGlyILEAsp 220
Db CTCAACCAAGTCTGAGTGTGGCTCTCTGCGAGGACACATTCATTGGAGATTCAGC 723
QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProILEanArgGluTyrTyrGlu 240
Db CACTGCTGTACACAGGAGTCTCTGTATACACCCATCCGCGGAGTGTATTATAGAG 783
QY 241 ValILEILEValArgValGluILEanGlyGlnAspLeuLysMetAspCysLysGluTyr 260
Db GTCATCATTTGGCGGTGAGATCATAGACAGATCTGAAATATGACTCCAGAGAGTAC 843
QY 261 AsnTyrAspLysSerILEValAspSerGlyThrThrAnLeuArgLeuProLysVal 280

Db 844 AACTATGACAGAGCATTTGTGACAGTGGACACCAACTTCTGTTGCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValLysSerILEuValAlaAspSerThrGluLysPheProAspGly 300
Db TTTGAAGCTGACAGTCAATTCATCAAGGACACCTCTCCAGGAAAGTTCCCTGATGGT 963
QY 301 PheTyrPLeuGlyGluGluILEuValCysTyrPheGlnIleGlyThrProTyrPheILEPhe 320
Db TTCTGGCTAGAGACACACTGTGTGTGCGACAGGACACACCCCTTGACATTTTC 1023
QY 321 ProValILESerLeuTyrLeuMetGlyGlyValThrAnGlnSerPheArgILEThrILE 340
Db CCAGTCATCTCACTCACTAATGAGTGAAGTTACCAACAGTCTCTCCGATCACCATC 1083
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db CTTCGACGCAATACCTGGGCGCAGTGAAGATGTGCCACGTTCCCAAGACGACTGTAC 1143
QY 361 LysPheAlaILESerGlnSerSerThrGlyThrValMetGlyAlaValILEMetGluGly 380
Db AAGTTGCACTCATCAGATATCCAGCGGCACTTTATGGAGCTTTATCATATGAGGGC 1203
QY 381 PheTyrValValPheAspArgAlaArgLysArgILEGlyPheAlaValSerAlaCysHIS 400
Db TTCTACGTTGTCTTGTGATCGGGCCCGAAACGAATGGCTTGTCTGTCAAGCGCTTGCAT 1263
QY 401 ValHISAspGluPheArgThrAlaAlaValILEGluGlyProPheValThrLeuAspMetGlu 420
Db GTGCACGATGATTCACAGACGCGACGCGTGAAGGCCCTTTGTGTCACTTGACATGAA 1323
QY 421 AspCysGlyTyrAnILEProGlnThrAspGluSerThr 433
Db GACTGTGGCTAACAACTTCCACAGACGATGATCAACC 1362

RESULT 9

US-09-548-373D-3

Sequence 3, Application US/09548373D

Patent No. 6737510

GENERAL INFORMATION:

APPLICANT: GURNEY ET AL.

TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: 29915/62808

CURRENT APPLICATION NUMBER: US/09/548,373D

CURRENT FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: US 60/155,493

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 09/404,133

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: PCT/US99/20881

PRIOR FILING DATE: 1999-09-23

PRIOR APPLICATION NUMBER: US 60/101,594

PRIOR FILING DATE: 1998-09-24

NUMBER OF SEQ ID NOS: 73

SOFTWARE: PatentIn version 3.1

SEQ ID NO 3

LENGTH: 2070

TYPE: DNA

ORGANISM: Homo sapiens

US-09-548-373D-3

Alignment Scores:

Pred. No.:	4,34e-257	Length:	2070
Score:	2267.00 <td>Matches:</td> <td>429</td>	Matches:	429
Percent Similarity:	99.31% <td>Conservative:</td> <td>1</td>	Conservative:	1
Best Local Similarity:	99.08% <td>Mismatches:</td> <td>3</td>	Mismatches:	3
Query Match:	99.08% <td>Indels:</td> <td>0</td>	Indels:	0
DB:	4	Gaps:	0

US-10-726-967A-84 (1-433) x US-09-548-373D-3 (1-2070)

QY 1 ThrGlnHISGlyILEArgLeuProLeuArgSerGlyLeuGlyGlyValAlaProLeuGlyLeu 20

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Db      64 ACCGACGACGGGATCCGGCTCCCTCCGACAGCGGCTGGGGGGGCCCCCTGGGGCTG 123
Qy      21 GIUIEAASMLEUGLUTHZAPGLUGLUPROGLUGLUPROGLIYARGGLYSERPHEVAL 40
      124 CGGCTGCCCGGGAGACGAGACGAGAGCGGAGAGCCCGGAGGGGGCAGCTTTGG 183
Qy      41 GIUMETVALASPAMLEUARGLYLYSERGLYGLINGLYTYRTRYVALGIUMETHRVAL 60
      184 GAGATGTGTGACAACTGAGGGGCAAGTCGGGGCAGGGGCTACTAGGTGAGTGCAGCG 243
Qy      61 GYSEPRPROGLTHRIEUBENILEUVALAPRTHGLYSESERASNPHEALVAL 80
      244 GGCACGCCCCCGACGCTCAACATCTGTGTGATACAGGACAGTAACTTTGACGTG 303
Qy      81 GIYALALAPROHISPROPHLEUWHISARGTYRTRYGLINARGLINLEUSERSERTHTRY 100
      304 GGTGCTGCCCGCCACCCCTTCTGTGATGCTACTACCAAGGACAGTGTCCAGACATAC 363
Qy      101 ARGAPLEUARGLYGLYVALTRYVALPROLYRTHRGLINGLYLYSTTPGLUGLUGLEU 120
      364 CGGGAAGCTCCGAGAGGGGTGTATGTGCTTACACCCAGGGCAAGTGGAGAGGGAGCTG 423
Qy      121 GYTHRAPLEUVALSERILEPROHISGLYPROASNPVALTHRVALARGALASNPHEAL 140
      424 GGCACCGACCTGTGTAGCATCCCGACGCGCCCAAGCTCATGTGCTGCCAATTCCT 483
Qy      141 ALAILETHGLUSERASNPHEPHEHLEASNGLYSERASNPTRPGULYILEUGLY 160
      484 GGCATCATCGAATCAGACAAAGTTCTTCATCAACGGCTCCACATCGGGAAGGACCTCG 543
Qy      161 LEUALATYRVALGLULLEALARGPROASNPASNPSERLLEUGLUPROPHEPHEASNP 180
      544 CTGGCTTAGTGTAGATGCTCCAGGCTGACGACTCCCTGAGGCTTTCTTGACTCTCTG 603
Qy      181 VALYVSGINTHHSIALPROASNPHEPHESERLLEUGLYAGLYPHEPRO 200
      604 GTAAGACAGACCCACCTTCCCACTTCTCTCCAGCTTGTGTGTGTGCTTCTCC 663
Qy      201 LEUASNPISERGLYVALLEUASNPASNPVALGLYGLYSERMETILEILEGLYGLY 220
      664 CTCACCAATCTGAATGCTGCTGCTGTGAGGAGGATGATCATTTGAGGATACGAC 723
Qy      221 HISERLEUTRYTHRGLYSERLLEUTRYRTHRPROILEARGRGLUTRTRYRGLU 240
      724 CACTCGCTGTACACAGGCACTCTGTGTATACACCATCCGCGGGAGTGTATTTGAG 783
Qy      241 VALILEILEVALARGVALGLULLEASNGLYGLINAPLEUWHISERASNPGLYVSG 260
      784 GTCATCATTTGTGGGTGTGAGATCAATGACAGGATCTGAAATGAGACTGCAAGAGTAC 843
Qy      261 AANTYRASPILYSERLILEVALASPSERLYTHRTHASNPARGLEUPROLYVSLYV 280
      844 AACTATGACAAAGCATTTGTGACATGGGCAACCACTTGTGTTGCCAAGAAAGT 903
Qy      281 PHEGLUALALAVALLYSERILEYVALIASERSETHRGLYVSPHEPROAPGLY 300
      904 TTTGAAGCTGCAATCAATCAATCAAGGCACTCTCCACGAGAAATTCCTGTAGTGT 963
Qy      301 PHEITPLEUGLYGLUGLILEUVALCYSTTPGLINAGLYRTHRPROTPANILEPE 320
      964 TTCTGCTAGAGAGCGCTGTGTCTGTGCAAGGAGGCAACCCCTTGGAACTTTTC 1023
Qy      321 PROVALIILESERLEUTRYLEUMETGLYVALIATHASNPINSERPHEARGILETHRI 340
      1024 CCACTCATCTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1083
Qy      341 LEUPROGLINTRYLEUARGPROVALIUNASNPVALIATHASERGLINASNPARG 360
      1084 CTTCGCGAGCAATACCTGCGGCAAGTGTGAGATGTGCGCCCAAGCAAGCTGTTC 1143
Qy      361 LYRPHALALILESERGLINSERLTHRGLYTHRVALMETGLYVALIILEMETGLY 380
      1144 AAGTTTGCATCTCAAGTATCAAGGAGCTGTATGAGGACGTGTATCAATGAGGAG 1203

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Qy      381 PHERYVALVALPHEASNPARGALARGLYARGGLILEGLYPHEALVALSERALCYBHIS 400
Db      1204 TTCTACGTTGCTTTGATCGGGCCCGAAGACAAATGCTTTGCTGTACGCGCTTGCA 1263
Qy      401 VALHISAPGLUPHEARGTHRVALALVALGLUGLYPROPHEVALTHRLEUASNPARG 420
      1264 GTGCAGATGAGTTTCAGACGCGGCAAGCGGTGGAAGGCCCTTTGTCACTTGTGACAT 1323
Qy      421 ASPCYSGLYTRYASNPILEPROGLINTHRAPGLUSERTHR 433
      1324 GACTGTGCTCAACATTCACAGACAGATGATGATCAACC 1362
Db
RESULT 10
US-09-795-847B-3
/ Sequence 3, Application US/09795847B
/ Patent No. 6753163
/ GENERAL INFORMATION:
/ APPLICANT: Guirney, Mark E.
/ APPLICANT: Bienkowski, Michael J.
/ APPLICANT: Helmikson, Robert L.
/ APPLICANT: Parodi, Luis A.
/ APPLICANT: Yan, Riqiang
/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
/ FILE REFERENCE: 28341/6280DE
/ CURRENT APPLICATION NUMBER: US/09/795,847B
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 09/416,901
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 2070
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-795-847B-3
Alignment Scores:
Pred. No.: 4,346-257 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 4 Gaps: 0
US-10-726-967a-84 (1-433) x US-09-795-847B-3 (1-2070)
Qy      1 THRGIMHISGLYILEARGLEUPROLEUARGSERGLYLEUGLYGLYALAPROLEUGLYLEU 20
      64 ACCGACGACGGGATCCGGCTCCCTCCGACAGCGGCTGGGGGGGCCCCCTGGGGCTG 123
Qy      21 GIUIEAASMLEUGLUTHZAPGLUGLUPROGLUGLUPROGLIYARGGLYSERPHEVAL 40
      124 CGGCTGCCCGGGAGACGAGACGAGAGCGGAGAGCCCGGAGGGGGCAGCTTTGG 183
Qy      41 GIUMETVALASPAMLEUARGLYLYSERGLYGLINGLYTYRTRYVALGIUMETHRVAL 60
      184 GAGATGTGTGACAACTGAGGGGCAAGTCGGGGCAGGGGCTACTAGGTGAGTGCAGCG 243
Qy      61 GYSEPRPROGLTHRIEUBENILEUVALAPRTHGLYSESERASNPHEALVAL 80
      244 GGCACGCCCCCGACGCTCAACATCTGTGTGATACAGGACAGTAACTTTGACGTG 303
Qy      81 GIYALALAPROHISPROPHLEUWHISARGTYRTRYGLINARGLINLEUSERSERTHTRY 100

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Db 304 GGTCTGCCCCCACCCTCTCTCATCGCTACTACAGAGGCGAGCTGTCCAGACATAC 363
Qy 101 ArgAspLeuArglyGlyValTyrValProTyrThrGlnGlyLeuTyrPheGluValLeu 120
Db 364 CGGAGACCTCCGGAGGGGTGTATGTGCTCCACACCAAGGCAAGTGGAGAGGGAGCTG 423
Qy 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 424 GGCACCACTGGTAAGCATCCGCCATGGCCCCCAACTCTGCTGCTGCAACATTTGCT 483
Qy 141 AlaIleThrGlnSerAspIlePhePheIleAsnGlySerAsnTyrPheGluValLeuGly 160
Db 484 GCCATCATGTAATAGACAACTTCTTCAACAGGCTCCAACTGGAGAGGCACTCGGG 543
Qy 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCTTATGCTGATGCTGACAGGCTGACGACTCCCTGGAGCTTTCTTGACTCTCTG 603
Qy 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
Db 604 GTAAAGCAAGACCAAGTCCCAACCTTCTCTCCAGCTTGTGTGTGTGTGTGTGTGTGT 663
Qy 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
Db 664 CTCACACAGCTGTAAGTGTGGCTGTGTGAGGAGGAGATGATCATTTGGAGCTATGAC 723
Qy 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
Db 724 CACTCGCTGACACAGGAGCTCTGTGTATACCACTCGGAGGAGTGTGTATATGAG 783
Qy 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuIleMetAspCysIleGluTyr 260
Db 784 GTCATCATTTGTGGGTGGAGATCATGACAGAGACTGTAATAATGAGACTGCAAGAGTAC 843
Qy 261 AsnTyrAspIleSerIleValAspSerGlyThrThrAsnLeuArgLeuProIleValVal 280
Db 844 AACCTATGACAAAGCATTTGTGACAGTGGCAACCACTTCCTTGTGCCAAGAAAGTG 903
Qy 281 PheGlnAlaAlaValIleSerIleValAlaSerSerThrGlnIlePheProAspGly 300
Db 904 TTTGAGCTGCACTCAATTCATCAAGGAGCGCTCTTCCACGAGAAAGTTCCTATGGT 963
Qy 301 PheTyrPheGlyGlnGlnLeuValCysTyrPheGlnAlaGlyThrThrProTyrAsnIlePhe 320
Db 964 TTCTGGCTAGAGAGAGCTGTGTGTCTGGCAAGAGGACCACTTCCTGGAACATTTTC 1023
Qy 321 ProValIleSerLeuTyrIleMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAATCATCTCACTCACTTAATGGGTGAGTTTACCAACAGTCTTCCTGCAACCATC 1083
Qy 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1084 CTTCCGAGACATACCTCGGCGCACTGGAGAGTGTGGCCACTCCCAAGACACTTTTAC 1143
Qy 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGlnGly 380
Db 1144 AAGTTTGCATCTCAAGTCAATCCAGGCACTGTTATAGGAGCTGTTATATGAGAGGC 1203
Qy 381 PheTyrValAlaPheAspArgAlaArgIleAspArgIleGlyPheAlaValSerIleCysHis 400
Db 1204 TTCTACGTTTGTCTTGAATCGGCGCAAAACGAATTTGCTTGTGTAGAGCTTGGCAT 1263
Qy 401 ValHisAspGluPheArgThrAlaAlaValGlnGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGCAAGATGATTCAGAGCGGCAAGGAGAGGCTTTTGTCACTTGGACATGGA 1323
Qy 421 AspCysGlyTyrThrIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTACCAATTCACAGACAGATGATGTCACAC 1362
RESULT 11
US-09-548-366F-3

/ Sequence 3, Application US/09548366F
/ Patent No. 6797487
/ GENERAL INFORMATION:
/ APPLICANT: GURNEY ET AL.
/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
/ FILE REFERENCE: 29915/6280F
/ CURRENT FILING DATE: US/09/548, 366F
/ PRIOR FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: Patencin version 3.1
/ SEQ ID NO 3
/ LENGTH: 2070
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-548-366F-3

Alignment Scores:

Score:	4.34e-257	Length:	2070
Percent Similarity:	2267.00	Matches:	429
Best Local Similarity:	99.31%	Conservative:	1
Query Match:	99.08%	Mismatches:	3
DB:	4	Indels:	0
		Gaps:	0

US-10-726-967a-84 (1-433) x US-09-548-366F-3 (1-2070)

Qy 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAlaProLeuGlyLeu 20
Db 64 ACCAGACAGGACATCCGGCTGCTCCCTGCGACGGGCTGGGGGGCGCCCCCTGGGGCTG 123
Qy 21 GluIleAsnLeuGlnThrAspGlnGluProGluGluProGlyArgArgIleSerPheVal 40
Db 124 CGGCTGCCCGGAGAGACCGACGAGAGCCGAGAGAGCCGGCGGAGGGGAGCTTTGTG 183
Qy 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
Db 184 GAGATGTGAGAACCTGAGGGGCAAGTGGGGCAAGGCTTACTACGTGAGATGACCGTG 243
Qy 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 244 GGCAGCCCCCGGAGAGCGTCAACATCTGTGTGATACAGGAGAGCATTTGCAATG 303
Qy 81 GlyAlaAlaProHisProPheLeuHisAlaGlyTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db 304 GGTGTGCTCCCGCACCCCTTCTGCACTGCTTACCAAGAGGAGCTGTCCAGACATAC 363
Qy 101 ArgAspLeuArglyGlyValTyrValProTyrThrGlnGlyLysTyrPheGluValLeu 120
Db 364 CGGAGACCTCCGGAGAGGTGTGTGTGCTTACACCAAGGCAAGTGGAGAGGGAGCTG 423
Qy 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 424 GGCACCACTGGTAAGCATCCGCCATGGCCCCCAAGTCACTGTGTGCTTCAACATTTGCT 483
Qy 141 AlaIleThrGlnSerAspIlePhePheIleAsnGlySerAsnTyrPheGluValLeuGly 160
Db 484 GCCATCATGTAATAGACAACTTCTTCAACAGGCTCCAACTGGAGAGGCACTCGGG 543
Qy 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCTTATGCTGATGCTGACAGGCTGACGACTCCCTGAGAGCTTTCTTGACTCTCTG 603
Qy 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200


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Db      604 GTAAGCAGACCCAGTTCCTTCTCTCCGACCTTGTGCTGCTGCTTCC
Qy      201 leuaenglnsergluvalleualaaserValgllysermetilellegllyleap
Db      664 CTCACACAGCTGAGAGTCTGCGCTCTGCGAGGAGCATATCATGAGATCCAC
Qy      221 HiserleutythrGllyserleutythrProllaArgArgluuProlytyrGlu
Db      724 CACTGCTGTACACAGGAGCTCTGTGTATACCCATCCGCGGAGGTGATATTATG
Qy      241 ValileleValArgValgluileanglylnaspleuLeuMetAspCyslysgluTy
Db      784 GTTCATCATTTGTGCGGTGAGATCAATGACAGATCTGAAAATGACCTGCAGAGTAC
Qy      261 AsnTYrAspLysSerileValAspSerGlyThrThrAsnLeuArgleuProlyVal
Db      844 AACTATGACAGAGCATTTGTGACAGTGGCACACCACTTCCTGTTGCCAAGAAAGT
Qy      281 PhegluaAlaVallyserlileValaAlaserSerThrGluLysPheProAspGly
Db      904 TTTGAAGCTGACGTCAATTCATCAAGGAGCCTCTCCACGAGAAATTCCTGATGAT
Qy      301 PheTrpleuGlygluInleuValCysTrpGlnAlaGlyThrThrProTrpAsnilePhe
Db      964 TTCTGCTGAGAGAGAGCTGTGTCTGCGACAGGACCACTCCCTGGAAATTTTC
Qy      321 ProvalileserleutythrleuMetGlygluValThrAsnGlnserPheArgileThr
Db      1024 CCAATCATCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT
Qy      341 leuProGlnGlnTyrlleuArgProValGluAspValAlaThrserGlnAspAspGly
Db      1084 CTTCCTCCACCAATACCTGCGGCGCAGAGGAGATGTGGCCACCTCCCAAGACATTTAC
Qy      361 LysPheAlaileserGlnserSerThrGlyThrValMetGlyAlaValileMetGly
Db      1144 AGTTGTCCATCTCACAGTATCACAGGAGCATGTTATGAGACCTTTATCATGAGGGC
Qy      381 PheTYrValValPheAspArgAlaArglyAsArgileGlyPheAlaValserAlaCysHis
Db      1204 TTCTACCTGTCTTGTATCGGCGCCGAAACGAATTTGGCTTCTGACGCTTGCAT
Qy      401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrleuAspMetGlu
Db      1264 GTGCAAGATGAGTTCAGGACGCGAGCGGTGAAAGGCCCTTTGTCTCACTTGACATG
Qy      421 AspCysGlyTYrAsnileProGlnThrAspGlnSerThr
Db      1324 GACTGTGGCTACAACTTCACAGACAGATGATCAACC

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RESULT 12
US-09-548-368D-3

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; Sequence 3, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
; APPLICANT: GUNNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280C
; CURRENT APPLICATION NUMBER: US/09/548,368D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2070

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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-548-368D-3
Alignment Scores:
Pred. No.: 4,346-257
Score: 2267.00
Percent Similarity: 99.31%
Best Local Similarity: 99.08%
Query Match: 99.08%
DB: 4
Gaps: 0
US-10-726-967A-84 (1-433) x US-09-548-368D-3 (1-2070)
Qy      1 ThrGlnHleGlylleArgleuProleuArgSerGlyleuGlyValaProleuGlyleu
Db      64 ACCGACAGCGGATCCGCTGCTGCGACAGGCGCTGGGCGGCCCTTGGAGCTG
Qy      21 GluileAsnleuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal
Db      124 CCGCTGCCCCGGAAGACGACAGAGAGCCCGAGAGCCCGCGGAGGCGAGCTTTG
Qy      41 GluMetValAspAsnleuArgGlyLysSerGlyGlnGlyTYrTYrValGluMetThrVal
Db      184 GAGATGTGAGCAACCTGAGGGGCAAGTCCGGGCGAGGCTACTACGTGAGATGACCGTG
Qy      61 GlySerProProGlnThrleuAsnileleuValAspThrGlySerSerAspPheAlaVal
Db      244 GGCACCCCCCCCAACAGCTCAACATCTGTGTGATACAGGAGGAGCATTAATTGCAATG
Qy      81 GlyAlaAlaProHisProPheleuHisArgTYrTYrGlnArgGlnleuSerSerThrTYr
Db      304 GGTGTGCCCCCACCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Qy      101 ArgAspLeuArgLysGlyValTYrValProTYrThrGlnGlyLysTrpGluGlyleu
Db      364 CGGAGCTCCGGAAGGCTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Qy      121 GlyThrAspLeuValSerileProHisGlyProAsnValThrValArgAlaAsnileAla
Db      424 GGCACGAGCTGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
Qy      141 AlaileThrGlnSerAspLysPhePheileAnglySerAsnTrpGluGlyleuGly
Db      484 GGCATCATGATTCAGACAGATTTCTTATCAACGGCTCCAACTGGAGAGCATTCCTGGG
Qy      161 leuAlaTYrAlaGluileAlaArgProAspAspSerleuGluProPhePheAspSerleu
Db      544 CTGGCTTATGCTGAGATTTGCCAGGCTGACGACTCCCTGAGGCTTTCTTGACTCTG
Qy      181 VallyGlnThrHisValProAsnleuPheSerleuGlnleuGlyAlaGlyPhePro
Db      604 GTAAGCAGACCCAGTTCCTTCCAACTCTCTCCGACCTTGTGCTGCTGCTTCC
Qy      201 leuaenglnsergluvalleualaaserValgllysermetilellegllyleap
Db      664 CTCACACAGCTGAGAGTCTGCGCTCTGCGAGGAGCATATCATGAGATCCAC
Qy      221 HiserleutythrGllyserleutythrProllaArgArgluuProlytyrGlu
Db      724 CACTGCTGTACACAGGAGCTCTGTGTATACCCATCCGCGGAGGTGATATTATG
Qy      241 ValileleValArgValgluileanglylnaspleuLeuMetAspCyslysgluTy
Db      784 GTTCATCATTTGTGCGGTGAGATCAATGACAGATCTGAAAATGACCTGCAGAGTAC
Qy      261 AsnTYrAspLysSerileValAspSerGlyThrThrAsnLeuArgleuProlyVal
Db      844 AACTATGACAGAGCATTTGTGACAGTGGCACACCACTTCCTGTTGCCAAGAAAGT
Qy      281 PhegluaAlaVallyserlileValaAlaserSerThrGluLysPheProAspGly
Db      904 TTTGAAGCTGACGTCAATTCATCAAGGAGCCTCTCCACGAGAAATTCCTGATGAT

```

QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrProTrpAsnIlePhe 320
Db 964 TTCTGGCTAGAGAGAGAGCTGTGTGTGGCAACAGCACACCCCTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTyrlLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAAGTCATCTCACTCACTCAATGAGGTTCACCAACCAAGTCCTTCCGACATCACATC 1083
QY 341 LeuProGlnGlnTyrlLeuArgProValGluAspValAlaThrSerGlnAspArgCysTyrl 360
Db 1084 CTTCGGACAAATACCTGGCGGCAAGTGAATGTGCCACGTCCCAAGACGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1144 AAGTTTGCCATCTCAACAGTCATCCACGGGCACTTTATGGAGCTGTATCATGAGGGC 1203
QY 381 PheTyrlValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1204 TTCTACCTGTGTCTTGTATCGGGCCGAAACGAATTGGCTTGTCTGTCAAGCGCTTCCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGACCATGAGTTCAGAGAGCGGACGGTGAAGGCCCTTTGTGTCACTTGACATGGAA 1323
QY 421 AspCysGlyTyrlAsnIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTAACAACTTCACAGACAGATGATCAACC 1362

RESULT 13
US-09-794-925A-3
/ Sequence 3, Application US/09794925A
/ Patent No. 6828117
/ GENERAL INFORMATION:
/ APPLICANT: Gurney et al.
/ TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
/ FILE REFERENCE: 29915/6280H1
/ CURRENT APPLICATION NUMBER: US/09/794,925A
/ PRIOR FILING DATE: 2001-02-27
/ PRIOR APPLICATION NUMBER: 09/416,901
/ PRIOR FILING DATE: 1999-10-13
/ PRIOR APPLICATION NUMBER: 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: 60/101,594
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 2070
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-794-925A-3

Alignment Scores:
Pred. No.: 4,34e-257 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 4 Gaps: 0

US-10-726-967a-84 (1-433) x US-09-794-925A-3 (1-2070)

QY 1 ThrGlnHisGlyTlArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
Db 64 ACCCGACACGGGATCCGGCTGGCCCTGGCGACGGGCTGGGGGGGCCCCCTGGGGCTG 123
QY 21 GluIleAsnLeuGluThrAspGluGluProGlnGluGluProGlnGlyArgArgIleSerPheVal 40

Db 124 CGGCTGCCCCGGGAAACCGACGAAAGAGCCCGAGGGCCGGAGGGGCGAGCTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrlValGluMetThrVal 60
Db 184 GAGATGTGTGACAACTTATGAGGGGCAAGTGGGGGAGGCTTCTACGTGAGATACCGTG 243
QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 244 GGCACGCCCCCGGACGCTCAACATCTGTGTGATACAGGACACAGAACTTTGGAGTG 303
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrlTyrlGlnArgGlnLeuSerSerThrTyrl 100
Db 304 GGTGTGCCCCCGACCCCTTCTGTCACTGCTTACACCAAGGCGAGCTGTCCAGCACATAC 363
QY 101 ArgAspLeuAlaGlyGlyValTyrlValProTyrlThrGlnGlyLysTrpGluGlyLeu 120
Db 364 CGGACCTCCGGAAAGGGTGTATATGTCCCTTACACCAAGGCGAAGTGGAAAGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 424 GGCACCGACCTGTGTAGCATCCCCCATGGCCCAAGCTCACTGTGCGTCCAAACATTTGCT 483
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerSerThrProGluGlyIleLeuGly 160
Db 484 GCCATCACTGATGACAGATTTTATCATACAGCTCCAACTGGGAAAGGCACTTGGGG 543
QY 161 LeuAlaTyrlAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180
Db 544 CTGGCTATGTGTGATTTGCCAGAGGCTGACGACTCCCTGGAGCTTCTTGTACTCTGTG 603
QY 181 ValLysGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro 200
Db 604 GTAAAGCAAGCCACGTTCCCAACTCTTCTCCCTGACGCTTGTGTGTGTGCTTCCCC 663
QY 201 LeuAsnGlnSerGluValIleAlaSerValGlySerMetIleIleGlyIleAsp 220
Db 664 CTCAACCAAGCTGAAGTGTGGCTGTCTGTGGAGGAGCATGATCTTGAAGTATCGAC 723
QY 221 HisSerLeuTyrlThrGlySerLeuTyrlTyrlProIleArgArgGluTrpTyrlGlu 240
Db 724 CACTGCTGTACACAGGAGTCTCTGTATACCACTCCGGGGGAGTGTATATGAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLysGlyTyrl 260
Db 784 GTCACTATGTGGGGGGGAGATCAATGACAGGATCTAAATGACATGCAAGGAGTAC 843
QY 261 AsnTyrlAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 844 AACATGACAAAGCATTTGTGACATGTGACCAACCAACCTTCTGTGCCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValLysSerIleLysAlaAlaSerSerThrGluLysPheProAspGly 300
Db 904 TTGAAAGCTGCAATCAATCAATCAAGCGAGCTCTCCACGGAAGATTCCTGATGAT 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
Db 964 TTCTGGCTAGAGAGAGAGCTGTGTGTGGCAACAGCACACCCCTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTyrlLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAAGTCATCTCACTCACTCAATGAGGTTCACCAACCAAGTCCTTCCGACATCACATC 1083
QY 341 LeuProGlnGlnTyrlLeuArgProValGluAspValAlaThrSerGlnAspArgCysTyrl 360
Db 1084 CTTCGGACAAATACCTGGCGGCAAGTGAATGTGCCACGTCCCAAGACGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1144 AAGTTTGCCATCTCAACAGTCATCCACGGGCACTTTATGGAGCTGTATCATGAGGGC 1203
QY 381 PheTyrlValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400

Qy	Db	Qy	Db
401	1204	421	1324
ValHsAPGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu	TTCAACGGTGTCTTTGAATCGGGCCCGAAACCAATATGGCTTGTGCTGACGCCCTTGCAT	AspCysGlyTyrTrpAsnLeuProGlnThrThrAspGluSerThr	GACTGTGGCTACATCATTTCCACAGACAGATGATGATACC
1264		433	1362
GTGCACGATGAGTTTCAGACGCGACGCGGTGGAAAGGCCCTTTTGTCACTTGACATGGAA			

RESULT 14

```

US-09-806-194A-3
1 Sequence 3, Application US/09806194A
2 Patent No. 6835565
3 GENERAL INFORMATION:
4 APPLICANT: Gurney, Mark E.
5 APPLICANT: Bienkowski, Michael J.
6 APPLICANT: Heimriksson, Robert L.
7 APPLICANT: Parodi, Luis A.
8 APPLICANT: Van, Rigtang
9 APPLICANT: Pharmacia & Upjohn Company
10 TITLE OF INVENTION: Alzheimer's Disease Secretase
11 FILE REFERENCE: 6177.P CP
12 CURRENT APPLICATION NUMBER: US/09/806-194A
13 CURRENT FILING DATE: 2001-09-17
14 PRIOR APPLICATION NUMBER: 60/101,594
15 PRIOR FILING DATE: 1998-09-24
16 NUMBER OF SEQ ID NOS: 49
17 SOFTWARE: PatentIn Ver. 2.0
18 SEQ ID NO 3
19 LENGTH: 2070
20 TYPE: DNA
21 ORGANISM: Homo sapiens
22 US-09-806-194A-3

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Alignment Scores:	
Pred. No.:	4.34e-257
Score:	2267.00
Percent Similarity:	99.31%
Best Local Similarity:	99.08%
Query Match:	99.08%
DB:	4
Length:	2070
Matches:	429
Conservative:	1
Mismatches:	3
Indels:	0
Gaps:	0

US-10-726-967A-84 (1-433) X US-09-806-194A-3 (1-2070)

OY	1	ThrglnhiegilylAkrgeupProleuAryseegilyleuGlyValaProleuGlyleu	20
Db	64	ACCCAGCAGGACATCCGGCTGGCCCGCAGCGGCTGGGGGGCCCCCTGGGGAGCTG	123
OY	21	GluileAenleuGlyluthzaBpGugluProGluGluProGlyAArgArgGlySerPheVal	40
Db	124	CGGCTGCCCCGGGAGACCGACAGAGCCCGAGAGACCCGGCCGGAGGGGACGTTTGTG	183
OY	41	GluMetValAspAsnleuArgGlylySerGlyGlnGlyTyrTyrValGluMetThrVal	60
Db	184	GAGATGTGACACACTCGAGGGGCAAGTCGGGCAAGGCTACCTGGAGAAAGACCGTG	243
OY	61	GlySerProProGlnThrIleuAsnIleleuValAspThrGlySerSerAsnPheAlaVal	80
Db	244	GGGAGCCCCCGGAGAGCGCTCAACATCTGTGGATACAGGACAGATTACTTGCAGTG	303
OY	81	GlyAlaAlaProHisProPheleuHisArgTyrTyrGlnArgIleuSerSerThrTyr	100
Db	304	GGGTGCTGCCGCCACCCCTTCCTCGATCGTATACAGAGGAGCGTGTCCAGACATATAC	363
OY	101	ArgAspIleuArglysglyValIlyrValProTyrThrGlnGlylysrPgluGlyGluIleu	120
Db	364	CGGAGCCTCCGGAAGGGTGTGTATGTGGCCCTACACCGAGGCAAGTGGGAGGGAGCTG	423
OY	121	GlyThrAspIleuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla	140
Db	424	GGACAGCACTGGTAAGATCCCCCATGGCCCCCAAGTCATCTGTGGTCCCAATTTGCT	483

QY	141	allehrngusertaplysphephellakanslyserantpjluglylleuengly	160
Db	484	GCACACTGATGACAGCAAGTTCTTATCAACGGCTCCACTGGAAAGCATCCTGGG	543
QY	161	LeuAATYrAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu	180
Db	544	CTGGCCTATGCTGAGATTGGACAGGCTGACAGACTCCCTGGAGCCCTTCTTGACTCTTG	603
QY	181	VallysglnthrHlevalProAsnLeuPheSerLeuGlnLeuCyGlyValAglyPhePro	200
Db	604	GTAAGAAGCAGACCCAGTCCCAACCTCTTCTCCCTGCGACGCTTGTGGCTGGCTTCC	663
QY	201	LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyIleAsp	220
Db	664	CTCAACCGCTGGAAGTCTGACCTGCTCTGTGGAGGACATGATCATTTGGAGTATCCAC	723
QY	221	HisSerLeuYrThrGlySerLeuTrpYrThrProIleArgArgGluTrpYrYrGlu	240
Db	724	CACCTGCTGTACACAGGACAGTCTCTGTATACACCACCCGCGGAGTGATATAG	783
QY	241	ValIleIleValArgValGluIleAsnGlyGlnAspLeuYrMetAspCyelysGluYr	260
Db	784	GTCATCATTTGGCGGGTGAGATCATGACAGCATCTGAAATGATGACTGCAGAGATAC	843
QY	261	AsnYrAspYrAspSerIleValAspSerGlyYrThrAsnLeuArgLeuProYrAspVal	280
Db	844	AACATATGACAAAGACATTTGTGACAGTGACACACCAACTTGTTGCCCAAGAAAGTG	903
QY	281	PheGluAlaValIleYrSerIleYrAspAlaAspSerThrGluYrAspPheProAspGly	300
Db	904	TTTGAAAGCTGCAGTCAATTCATCAAGCAAGCTCTCCACGGAAGAGTTCCCTGATGGT	963
QY	301	PheTrpLeuGlyGluGlnLeuValCyserTrpGlnAlaGlyYrThrProTrpAsnIlePhe	320
Db	964	TTCTGGCTAGAGAGACAGCTGGTGTGTGCTGGCAAGACAGCACCACTTGGAAATTTTC	1022
QY	321	ProValIleSerLeuYrIleuMetGlyGluValIleTrpAsnGlnSerPheArgIleThrIle	340
Db	1024	CCAGCATCTCACTTACCTAATGAGGTGAGTTACCAACAGTCTTCCGATCACATC	1082
QY	341	LeuProGlnGlnYrIleuArgProValGluAspValAlaThrSerGlnAspAspCyYrYr	360
Db	1084	CTTCCGACGACATTACTGGCGGCAATGAAAGTGTGCCACGTCCCAACAGCATGTTC	1144
QY	361	IysPheAlaIleSerGlnSerSerThrGlyYrValMetGlyAlaValIleMetGluGly	380
Db	1144	AGTTTGCATCTCAACATCATCCACGGGCACTGTTATGGAGAGCTGTATCATGAGGGC	1202
QY	381	PheYrValValPheAspArgAlaArglyValArgIleGlyPheAlaValSerAlaCyHis	400
Db	1204	TTCTACGTTGCTTTGATCGGGCCGCAAAACAAATTTGGCTTGTGCTGACGGCTTGCCAT	1262
QY	401	ValIleAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu	420
Db	1264	GTGCACGATGAGTTCCAGCGGCAAGCGGTGGAAAGCCCTTTTGTCTCATTTGGACATGGAA	1322
QY	421	AspCyGlyYrYrAsnIleProGlnThrAspGlnSerThr	433
Db	1324	GACTGTGGTACAACTTCCACAGACAGATGAGTCAACC	1362
RESULT 15			
US-09-724-566A-42			
; Sequence 42, Application US/09724566A			
; Patent No. 6627739			
; GENERAL INFORMATION:			
; APPLICANT: Anderson, John P.			
; APPLICANT: Basi, Gurigdal			
; APPLICANT: Doane, Minh Tam			
; APPLICANT: Frigon, No. 6627739mand			
; APPLICANT: John, Varghese			
; APPLICANT: Power, Michael			
; APPLICANT: Sinha, Sukanto			
; APPLICANT: Tateuno, Gwen			

RESULT 15

US-09-724-566A-42
Sequence data, Application US/09724566A
Patent No. 6627739
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Bassi, Gurrigdal
APPLICANT: Doane, Minh Tam
APPLICANT: Frison, No. 6627739mand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Simha, Sukanto
APPLICANT: Tateano, Gwen

APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE OF INVENTION: Methods
FILE REFERENCE: 228-US-NEWC2
CURRENT APPLICATION NUMBER: US/09/724,566A
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/501,708
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: 60/119,571
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/139,172
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 42
LENGTH: 2348
TYPE: DNA
ORGANISM: Homo sapiens
US-09-724-566A-42

Alignment Scores:
Pred. No.: 5,33e-257 Length: 2348
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0
US-10-726-967a-84 (1-433) x US-09-724-566A-42 (1-2348)

QY 1 THRGHNLHAGLYTLAARGLEUPROLEWARGSERGLYLEGLVALAAROLENGLYLEU 20
DB 369 ACCGAGCAGGAGATCCGCTGCCCTGCGCAGCGGCTGGGGGCGCCCTTGAGGCTG 428
QY 21 GIULEAENLEUGLTHRAAPGLUGLUPROGLUGLUPROGLYARARGLYSERPHEVA 40
DB 429 CGGCTGCCCGGGAAGACCAAGAGAGCCGAGAGCCCGGAGGGGCGAGCTTTGTG 488
QY 41 GIUMETVALAPAPNLEUARGLYLYSERGLYGLINGLYTYRTRYVALGIUMETRYVA 60
DB 489 GAGATGATGACAACTGAGGGGCAAGTGGGGGAGGCTACTAGTGAGATGACCGTG 548
QY 61 GLYSERPROFROGLINTHRIEUAENLLEUVALAAPTTHRGLYSERSEANPHEHVA 80
DB 549 GGCACGCCCCCGACAGCGCTCAACATCCGTGATGATACAGGACAGTAACCTTTCAGTG 608
QY 81 GIYALALAPROHAPROPHLEUHIARGTYRTRYGLNARGGLNLEUSERSETHRTYR 100
DB 609 GGTGCTGCCCGCCACCCCTTCTGCACTGCTACTACAGAGGCACTGTCCAGCATAC 668
QY 101 ARGAPLEUARGLYGLYVALTRYVALPROLYRTHRGINGLYLYETRPGLUGLYLEU 120
DB 669 CGGAGACTCCGGAGAGGTGTATGTGCCCTACACCCAGGCAAGTGGAGAGGAGCTG 728
QY 121 GLYTHRAAPLEUVALSERILEPROHISGLYPROAENVALTHRVALARGALASNLLEA 140
DB 729 GGCACCGACCTGTGATGACATCCCGACAGCTCACTGCTGCTGCTGCTGCTGCT 788
QY 141 ALALETIRGLUSERASPLAPHEPHEILEANGLYSERASENTRGLUGLYILEUGLY 160
DB 789 GCCACACTGATGACAGCAAGTTCTTCATCAACGCGCTCCACTGGAGAGGCACTCTGGGG 848
QY 161 LEUALATYRALAGLILLEALARGPROAPAPSERLEUGLUPROPHENAPSERLEU 180
DB 849 CTGGCTATGCTGAGATGCTGAGGCTGACGACTCCCTGAGACTTTCTTGACTCTCTG 908
QY 181 VALLYSGINTHRIEVALPROAENLEUPHESERLEUGLNUCYGLYALAGLYPHEPRO 200
DB 909 GTAAAGACGACCAAGTGTCCCAACTTCTTCTCCGACGCTTGTGTGCTGGCTTCC 968
QY 201 LEUAENGLISERGLVALLEUALASERVALGLYGLYSERMETILEILEGLYGLYLEASP 220

DB 969 CTCACAGCTGTGAAGCTGCTGCTGTGCGAGGAGCATGATCATTTGAGGATGAC 1028
QY 221 HISSELEUTRYTHRGLYSERLEUTRPTRYTHRPROILEARGAGLUTTRYTYRGLU 240
DB 1029 CACTGCTGTACACAGGAGCTCTGGTATACACCCATCCCGCGGAGTGATATTATGAG 1088
QY 241 VALLEILEVALAVALAGLILLEANGLYGINAPLEUWMBETAPCYELVAGLYTYR 260
DB 1089 GTGATCATTTGCGAGTGAATGACATGACAGGATCTGAAAATGACTGCAAGGATAC 1148
QY 261 AENYRASPPLYSERILEVALASPSEGLYTHRTHRAENLEUARGLEUPROLYLYEVA 280
DB 1149 AACRTGACAGAGCATTTGTGACAGTGGACCAACCACTTCTGTTGCCAABAAAGTG 1208
QY 281 PHEGLUALAVALLYSERILEYALALASERSETHRGILYSPHEPROAPGLY 300
DB 1209 TTGAGAGCTGACAAATCCATCAAGGAGCCCTCCACGAGAAAGTTCCCTGATGCT 1268
QY 301 PHETRPLEUGLYGLUGLNUVALCYETRPGLNALGLYTHRPROTPAPENILEPHE 320
DB 1269 TTCTGGCTAGGAGAGAGCTGTGTGCTGGCAGACAGACACACCCCTTGAGACATTTTC 1328
QY 321 PROVALIISERLEUTRYLEUMERGILYGLUVALTHRAENGLISERPHENARGILETHRILE 340
DB 1329 CCACTCATCTCATCTACCTACCTTAATGGGTGAGGTTACCAACAGTCTCCGATCACATC 1388
QY 341 LEUPROGLINGLTRYLEUARGPROVALGLUAPYVALATHRSEGLINAPAPCYETRY 360
DB 1389 CTTCCGAGCAATACCTGCGGCCAGTGGAAAGATGTGCCACAGTCCCAAGACGACTGTTAC 1448
QY 361 LYPHEALALIESERGLISERSETHRGLYTHRVALMERGLYALVALILEMERGLUGLY 380
DB 1449 AAGTTGCACTCACTACAGTCACTCAAGGACCTGTATGAGAGCTGTATCATGAGAGGC 1508
QY 381 PNEYTRYVALVALPHEAPARGALAAAGLYAARGILEGLYPHEALVALSERALACYEHLIS 400
DB 1509 TTTACGTTGTCTTTGATCCGGGCCCGAAAACGAATTTGGCTTTGCTGCAAGGCTTGCAT 1568
QY 401 VALHISAPGLUPHEAAGTHRALALVALAGLUGLYPROPHEVALTHRLEUAPMERGLU 420
DB 1569 GTGACCATGATGTTCAAGACCGGACGGGTGGAAGGCCCTTTTGTCACTTGACATGAGAA 1628
QY 421 ASPCYGLYTRYAENLIEPROGLINTHRAAPGLUSERTHR 433
DB 1629 GACTGTGCTACAACTTCCACAGACAGATGATCAACC 1667

Search completed: August 22, 2005, 05:09:29
Job time : 327 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2005, 00:21:44 ; Search time 980 Seconds
(without alignment)
2615.559 Million cell updates/sec

Title: US-10-726-967a-84

Perfect score: 2288

Sequence: 1 TQHGRLRLPLRSGLGAPLGL.....FTVLMDGCGINIFQTEEST 433

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4330206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US10726667 @CGN 1.1.708 @runat.19082005.201239.29613 -NCPV=6 -ICPU=3
-NO MAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq.16Dec04:*
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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2267	99.1	1371	9 ACC84850	ACC84850 Human pro
2	2267	99.1	1503	3 AAA28278	AAA28278 Human CDN
3	2267	99.1	1503	3 AAA59550	AAA59550 DNA encod
4	2267	99.1	1506	9 ACC84849	ACC84849 Human mem
5	2267	99.1	1506	10 ADL18183	ADL18183 Human APP

6	2267	99.1	1524	13 ADQ82259	Adq82259 Human BAC
7	2267	99.1	1527	6 ABA02406	ABA02406 FLAG-tag
8	2267	99.1	1527	12 ADJ17857	Adj17857 Human CDN
9	2267	99.1	1527	12 ADP74534	Adp74534 Human ind
10	2267	99.1	1542	12 ADH34044	Adh34044 Human CDN
11	2267	99.1	2070	12 ADH94315	Adh94315 Human CDN
12	2267	99.1	2070	12 ADG50411	Adg50411 Human asp
13	2267	99.1	2070	13 ADP75324	Adp75324 Human asp
14	2267	99.1	2348	3 AAA59551	AAA59551 DNA encod
15	2267	99.1	2907	5 AAS82237	Aas82237 DNA encod
16	2267	99.1	3252	4 AAF28101	Aaf28101 Memapsin
17	2267	99.1	3252	4 AAF31848	Aaf31848 Human mem
18	2267	99.1	3252	6 ABR91244	AbR91244 Human CDN
19	2267	99.1	3252	6 ABR86641	AbR86641 CDNA enco
20	2267	99.1	3252	8 ABX11591	Abx11591 Human par
21	2267	99.1	3252	9 ADH74616	Adh74616 Human mem
22	2267	99.1	5832	12 ADP44628	Adp44628 Human bet
23	2267	99.1	5876	12 ADQ22186	Adq22186 Human sof
24	2267	99.1	5878	12 ADG86621	Adg86621 Human APP
25	2267	99.1	5878	12 ADQ17467	Adq17467 Human sof
26	2267	99.1	1368	12 ADJ57772	Adj57772 DNA seque
27	2267	99.1	2070	3 AAA15662	AAA15662 Human asp
28	2267	99.1	2070	4 AAS11702	Aas11702 DNA encod
29	2267	99.1	2070	4 AAD17865	Aad17865 Human asp
30	2267	99.1	2070	4 AAD13021	Aad13021 Human asp
31	2267	99.1	2070	4 AAD06739	Aad06739 Human asp
32	2267	99.1	2070	4 AAS11517	Aas11517 Human CDN
33	2267	99.1	2070	6 AB149914	Ab149914 Human asp
34	2267	99.1	2070	6 AB152457	Ab152457 Human asp
35	2267	99.1	2541	2 AAV41696	AAV41696 Nucleotid
36	2259	98.7	1368	12 ADJ57778	Adj57778 DNA seque
37	2257	98.6	1302	3 AAA15670	AAA15670 Human-pro
38	2257	98.6	1302	4 AAS11713	Aas11713 DNA encod
39	2257	98.6	1302	4 AAD17876	Aad17876 Human-pro
40	2257	98.6	1302	4 AAD13032	Aad13032 Human-pro
41	2257	98.6	1302	4 AAD06750	Aad06750 Human-pro
42	2257	98.6	1302	4 AAS11528	Aas11528 Human CDN
43	2257	98.6	1302	6 AB152468	Ab152468 Human-pro
44	2257	98.6	1302	12 ADJ94337	Adj94337 Human-pro
45	2257	98.6	1302	12 ADQ50433	AdQ50433 Human-pro

ALIGNMENTS

RESULT 1	ACC84850	standard; DNA; 1371 BP.
XX	ACC84850;	
AC	12-SEP-2003	(first entry)
XX		
DT		
DE	Human promemapsin 2-T1 protein encoding DNA.	
KW	Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;	
KW	beta-amyloid protein; Alzheimer's disease; promemapsin 2-T1; human; gene;	
KW	ds.	
OS	Homo sapiens.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	1..1371
FT		/tag= a
XX		/product= "promemapsin 2-T1"
XX		
PN	WO2003039454-A2.	
XX		
PD	15-MAY-2003.	
XX		
XX	23-OCT-2002; 2002WO-US034324.	
PF		
XX	23-OCT-2001; 2001US-035952P.	
PR	27-NOV-2001; 2001US-0333545P.	

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PR 14-JAN-2002; 2002US-0348464P.
PR 14-JAN-2002; 2002US-0348461SP.
PR 20-JUN-2002; 2002US-0390804P.
PR 19-JUL-2002; 2002US-0397557P.
PR 19-JUL-2002; 2002US-0397619P.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNII ) UNIV ILLINOIS FOUNO.
XX
PI Ghosh AK, Tang J, Bliceer G, Chang W, Hong L, Koelsch G, Loy J;
PI Turner RT;
XX
XX WPI; 2003-541410/51.
DR P-PSDB; ABR61929.
XX
PT New peptide compounds are memapsin beta secretase inhibitors used for
PT treating Alzheimer's disease.
XX
PS Example; Fig 10; 407pp; English.
XX
CC The invention relates to peptide compounds of specified formula. The
CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a human promemapsin 2-T1 protein encoding DNA
XX
SQ Sequence 1371 BP; 292 A; 395 C; 400 G; 284 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.8e-227 Length: 1371
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 9 Gaps: 0

US-10-726-967a-84 (1-433) x ACC84850 (1-1371)

QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
Db 70 ACCCAGACGGGCACTCGGGCTGCCCTCCGACGGGCTGGGGGCGCCCTTGGGGCTG 129
QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
Db 130 CGGCTCCCGGGAGAGCCAGCAGAGAGCCGAGAGCCCGGCGGAGGGGCGCTTGG 189
QY 41 GluMetValAspAsnLeuArgGlySerGlyGlnGlyTyrTyrValGluMetThrVal 60
Db 190 GAGATGCTGACAACTGAGGGGCAAGTCGGGGCAGGGCTACTACGTGAGATGACCGTG 249
QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 250 GGCAGAGCCCGCCAGACGCTCAACATCCGTGGTGAACAGGACAGTAAGTAACCTTGCATG 309
QY 81 GlyAlaIleAlaProHisProPheLeuHisArgGlyTyrGlnArgGlnLeuSerSerThrTyr 100
Db 310 GGTGTGCGCCCGCCACCCCTTCTCTGATGCTACTACCAAGAGCCACACTGTCACGACATAC 369
QY 101 ArgAspLeuArgGlyGlyValTyrValProTyrThrGlnGlyLysThrGlnGlyLeu 120
Db 370 CGGAGCCTCCGGAAGGGTGTGTATGTGCTTACACCCAGGGCAAGTGGAAAGGGAGCTG 429
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 430 GGCACCGACCTGTGTAAAGATCCCATGAGCCCAACGTCATCTGTCGCGCAACTTGGCT 489
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTyrGluGlyIleLeuGly 160
Db 490 GGCATCATCTGAATCAGACAAAGTCTTCTCAACACGCTCAACTGAGAAAGGCAATCTGAGG 549
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 550 CTGGCTATGCTGAGATTGCCAGGCTTACGACTCTCCCTGGAGCCTTCTTTGACTCTCTG 609

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QY 181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
Db 610 GTAAAGCAGACCCACAGTTCCTCCAACTCTTCTCCGACGCTTTGGGCTGGCTTCCCC 669
QY 201 LeuAsnGlnSerGluValIleuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
Db 670 CTCAACCAAGTCTGAAGTCTGGCTCTGTGCGAGGAGCATGATCATTTGAGGATATGAC 729
QY 221 HisSerLeuTyrThrGlySerLeuTyrThrProIleArgGluTyrTyrGlu 240
Db 730 CACTGCTGTACACAGCGAGTCTGTGTATACCCATCCCGCGGAGTGTATTATAGAG 789
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCyLysGluTyr 260
Db 790 GTCATCATTTGCGGGGTGAGATCAATGACAGATCTGAATAATGACTGCAGAGATAC 849
QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 850 AACTATGACAAAGACATTGTGACAGTGGCACACCAACCTTGCTTGGCCCAAGAAAGTG 909
QY 281 PheGluAlaIleValLysSerIleLysAlaIleSerSerThrGluLysPheProAspGly 300
Db 910 TTGAAAGCTGACGTCMAATCATTCATTAAGGCAAGCTCTCTCCAGGAGAAAGTTCCTGATGT 969
QY 301 PheTyrLeuGlyGluGlnLeuValCysTyrGlnAlaGlyThrThrProTyrAsnIlePhe 320
Db 970 TTCTGGCTAGAGAGACAGTGTGTCTGTGCAAGACAGCAACCCCTTGAAATTTTC 1029
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1030 CCAAGTATCTCACTTCACTTAATGGGTGAAGTTTACCAACCAAGTCTTCCGATCACCATC 1089
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1090 CTTCCGACAGCAATACCTGGCGCCAGTGAAGATGTGTGCCACGCTCCCAACACACTTTAC 1149
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyValAlaIleMetGluGly 380
Db 1150 AAGTTTGCCATCTCAACATCATCCAGGCGACCTGTATGTGAGTGTATCATGAGGGGC 1209
QY 381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerIleCysHis 400
Db 1210 TTCTACGTTGTCTTTGATCGGGCCCAAAACGAATGGCTTTGTGCTGACGCTTGCCAT 1269
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1270 GTCCACGATGAGTTCAAGACGGCAGCGGTGAAGGCCCTTTGTGTACCTTGGACATGGAA 1329
QY 421 AspCysGlyTyrTyrAsnIleProGlnThrAspGluSerThr 433
Db 1330 GACTGTGGCTTACAACTTCCACAGACAGATGAGTCAACC 1368

RESULT 2
AAA28278
ID AAA28278 standard; cDNA; 1503 BP.
XX
AC AAA28278;
XX
XX 12-FEB-2001 (first entry)
XX
DE Human cDNA encoding beta-secretase.
XX
XX Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease; human;
XX Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective; ss.
XX
OS Homo sapiens.
XX
XX Key 1.1503
XX CDS Location/Qualifiers
XX
FT 1..1503
FT /tag= a
FT /product= "Beta secretase"
FT /note= "No stop codon given"

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Db 1324 GACTGTGGCTTCAACATTTCCACAGACAGATGATCAACC 1362

RESULT 3
ID AAAA59550
AAA59550 standard; DNA; 1503 BP.
XX
AC AAA59550;
XX
DT 14-NOV-2000 (first entry)
XX
DE DNA encoding a human beta-secretase enzyme.
XX
KM Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KM amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KM inhibitor; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1503
FT /tag= a
FT /product= "beta-secretase"
FT /note= "no termination codon given"
XX
PN MO200047618-A2.
XX
PD 17-AUG-2000.
XX
PF 10-FEB-2000; 2000MO-US003819.
XX
PR 10-FEB-1999; 99US-0119571P.
PR 15-JUN-1999; 99US-0139172P.
XX
PA (ELAN-) ELAN PHARM INC.
PI Anderson JP, Basl G, Doane MT, Frigon N, John V, Power M,
PI Sinha S, Tatsuno G, Tung J, Wang S, Mcconlogue L,
DR WPI; 2000-533011/48.
XX P-PSDB; AAB07896.
PT Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.
XX
PS Disclosure; Fig 1A; 121pp; English.
XX
CC The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC encodes a human beta-secretase enzyme
XX
SQ Sequence 1503 BP; 305 A; 448 C; 431 G; 319 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,04e-227 Length: 1503
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0

US-10-726-967a-84 (1-433) x AAA59550 (1-1503)

QY 1 ThrGlnHsGlyIleArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
|||||

Db 64 ACCGACACGGGCTGCGCCCTGCGCAGCGGCTGCGGCGGCGCCCTGCGGCGCTG 123

QY 21 GluIleAmLeuGlyThrAspGluGluProGluGluProGlyIleArgAspGlySerPheVal 40
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Db 124 CGGCTGCCCGGGAGACCGACGAGAGAGCCCGAGAGCCCGGAGGAGCGCTTGTG 183

QY 41 GluMetValAspAmLeuArgGlyIleSerGlyGlnGlyIleValGluMetThrVal 60

Db 184 GAGATGGTGGACAACCTGAGGGGCAAGTCGGGGGCGAGGCTACTACGTGAGATGACCGTG 243

QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAspPheAlaVal 80

Db 244 GCGAGCCCCCGGAGACGCTCAACATCTGAGTATACAGGACAGTAACTTTGCGAGTG 303

QY 81 GlyAlaAlaProHisProPheLeuHisArgGlyIleArgGlnLeuSerSerThrTyr 100

Db 304 GGTGTGCCCCCGACCCCTTCTGATGCTACACAGAGGAGCGCTGTCCAGACATAC 363

QY 101 ArgAspLeuArgGlyGlyValIleTyrValProTyrThrGlnGlyIleTyrGluLeu 120

Db 364 CGGAGACCTCCGAGAGGGGTGTGTATGTGCTTACACCCAGGCGCAAGTGGAGGAGAGCTG 423

QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValAspAlaAsnIleAla 140

Db 424 GGCACCGACCTGTGACGATCCCGCATGGCCCGCAACGTACTGTGCGCCAGCATTTGCT 483

QY 141 AlaIleThrGluSerAspIlePhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160

Db 484 GCCATCACTGAAATGACAGCAAGTTCTTCATCAACGGCTCCAACTGGGAGGCACTCTGGG 543

QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180

Db 544 CTGGCTATGTGTGATGTGCGAGGCTGACGACCTCCCTGAGGCTTTCTTGTGACTCTG 603

QY 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro 200

Db 604 GTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGAGCTTGTGTGCTGCTTCC 663

QY 201 LeuAsnGlnSerGlyValIleAsnIleSerValGlyIleSerMetIleIleGlyIleAsp 220

Db 664 CTCAACGAGCTGAAAGCTGGGCTCTGTGCGAGGAGCATGATCATTTGAGGATGAG 723

QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240

Db 724 CACTCGCTGACAGGAGCACTCTGTGATACCCATCCGCGGAGGTGTATTTATGAG 783

QY 241 ValIleIleValIleArgValGluIleAsnGlyGlnAspLeuIleMetAspCysIleGlyTyr 260

Db 784 GTGATCATTTGTGGGGTGGAGATCAATGACAGATCTGMAAATGACATGCAAGAGGTTC 843

QY 261 AsnTyrAspIleSerIleValAspSerGlyThrThrAsnLeuArgLeuProIleValVal 280

Db 844 AACCTAGACAGAGCAATGTGGACAGTGGACACCAACCTTGTGTGGCCAAAGAAAGTG 903

QY 281 PheGluAlaAlaValIleSerIleIleValAlaIleSerSerThrGluIlePheProAspGly 300

Db 904 TTGGAGCTGCATCAATCAATCCATCAAGGACCTCTCCACGAGAGAGTTCCCTGATGTT 963

QY 301 PheIlePheGlyGlyGlnLeuValCysTrpGlnAlaGlyIleThrThrProTrpAsnIlePhe 320

Db 964 TTCTGTGCTAGAGAGAGCTGTGTGCTGCAAGGACGACACCCCTTGGAACATTTTTC 1023

QY 321 ProValIleSerLeuTyrLeuMetGlyValIleThrAsnGlnSerPheArgIleThrIle 340

Db 1024 CCGATATCTCACTCACTCAATATGGGTGGTTTACCAACCACTCTTTCGCAATCCACATC 1083

QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360

Db 1084 CTTCCGACACCAATACCTGGCGGCAGTGGAAAGTGTGCCAGCTCCCAAGACACATCTTAC 1143

QY 361 IysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380

Db 1144 AAGTTTGCATCTCAACATCATCCAGGGCACTGTTATGGAGCTGTATCATGAGAGGC 1203

Qy	381	hethYrrValValPheAspArgAlaArgIysArgIleGlyPheAlaValSerIaCysHis	400
Db	1204	TTCTACGTTGCTTTGATCGGGCCCGAAAAACAATTGGCTTGTCTGTACGGCTTGCAT	126
Qy	401	ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu	420
Db	1264	GTGCACGATGAATTCCAGACGGCAGGGTGGAAAGGCCCTTTGTACCTTGGACATGGAA	132
Qy	421	AspGlyGlyTyrAsnIleProGlnThrAspGluSerThr	433
Db	1324	GACTGTGGCTACACATTCACATTCACAGACAGATGAGTACACC	1362
RESULT 4			
ACC84849			
ID	ACC84849	standard; DNA; 1506 BP.	
AC	ACC84849;		
XX			
DT	12-SEP-2003	(first entry)	
XX			
DE	Human memapsin 2 protein encoding DNA.		
XX			
KW	Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;		
KW	beta-amyloid protein; Alzheimer's disease; human; gene; de.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FH	CDS	1..1506	
FT		/*tag= a	
FT		/product= "memapsin 2"	
FT	sig_peptide	1..63	
FT		/*tag= b	
FT	mat_peptide	64..1503	
FT		/*tag= c	
XX			
PN	WO2003039454-A2.		
XX			
PD	15-MAY-2003.		
XX			
PR	23-OCT-2002;	2002WO-US034324.	
XX			
PR	23-OCT-2001;	2001US-0335952P.	
PR	27-NOV-2001;	2001US-0333545P.	
PR	14-JAN-2002;	2002US-0348464P.	
PR	14-JAN-2002;	2002US-0348615P.	
PR	20-JUN-2002;	2002US-0390804P.	
PR	19-JUL-2002;	2002US-0397557P.	
PR	19-JUL-2002;	2002US-0397619P.	
XX			
PA	(OKLA-) OKLAHOMA MEDICAL RES FOUND.		
PA	(UNIT) UNIT ILLINOIS FOUND.		
XX			
PI	Ghoesh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;		
PI	Turner RT;		
XX			
XX	WPI, 2003-541410/51.		
DR	P-PDSB; ABR61928.		
XX			
PT	New peptide compounds are memapsin beta secretase inhibitors used for		
PT	treating Alzheimer's disease.		
XX			
PS	Claim 101; Fig 8; 407pp; English.		
XX			
CC	The invention relates to peptide compounds of specified formula. The		
CC	compounds exhibit memapsin 2-beta secretase inhibitory activity relative		
CC	to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid		
CC	protein. The compounds can be used for treating Alzheimer's disease. The		
CC	present sequence represents a human memapsin 2 protein encoding DNA		
CC	(Genbank Index (GI):21040369)		
XX			
XX	Sequence 1506 BP; 306 A; 449 C; 431 G; 320 T; 0 U; 0 Other;		

Alignment Scores:		Pred. No.:	2.05e-227	Length:	1506
Score:	2267.00	Matches:	429		
Percent Similarity:	99.31%	Conservative:	1		
Best Local Similarity:	99.08%	Mismatches:	3		
Query Match:	99.08%	Indels:	0		
DBs:	9	Gaps:	0		
US-10-726-967A-84 (1-433) x ACC84849 (1-1506)					
QY	1	ThrglnHsgYlLeaArgLeuProLeuArgSerGlyLeuGlyGlyAlaProLeuGlyLeu	20		
DB	64	ACCACGACACGGCATCCGGCTGGCCCTGGCGACGGCCCTGGGGGGGGCCCCCTGGGGCTG	123		
QY	21	GluIleuLeuLeuGlnThrAspGlnGluProGluGluProGlyValArgGlySerPheVal	40		
DB	124	CGGCTGCCCCCGGAGAACCGACGAAAGGCCCGAGGAGCCGGCGGAGGGGACGCTTTGG	183		
QY	41	GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyYrYrValGluMetThrVal	60		
DB	184	GAGATGGTGGACAACTGAGGGGCAAGTGGGGCGAGGGGTACTAGTGGAGATGACCGTG	243		
QY	61	GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal	80		
DB	244	GGCAGCCCCCGACAGCTCAACTCCGTGGATACAGCAGCAGATGAATCTTGACATG	303		
QY	81	GlyAlaAlaProHisProPheLeuHisAsnGlyYrYrGlnAsnGlnLeuSerSerThrYr	100		
DB	304	GGTGTGCCCCCGACCCCTCTCGATGGCTACTACAGAGCAGCTGTCCAGCATAC	363		
QY	101	ArgAspLeuArgLysGlyValTyrValProYrThrGlnGlyLysIleTrpGluGlyLeu	120		
DB	364	CGGAGCTCCGGAAGGGTGTGATGTGGCTTACCCAGGGCAGAGTGGAGGGAGGCTG	423		
QY	121	GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla	140		
DB	424	GGCAGCGACCTGGTAAAGCATCCCGCATGGCCCCCAAGTCACTGTGGTGCACCAATGTCT	483		
QY	141	AlaIleThrGlyLysSerAspLysPhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly	160		
DB	484	GGCATCATCGAATTCAGACAAAGTTCTTCATCAACGGCTCCAACTGGAGAGCATCTCGGG	543		
QY	161	LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu	180		
DB	544	CTGGCTATGCTGAGATTGCCAGGCTGACGCTCCCTGAGGCTTCTTGACTCTG	603		
QY	181	ValIlyeGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro	200		
DB	604	GTAAGCAGACCCACGTTCCCAACCTCTCCCTGACGCTTGTGTCTGGCTTCCCC	663		
QY	201	LeuAsnGlnSerGluValLeuAlaSerValGlyLysMetIleIleGlyGlyIleAsp	220		
DB	664	CTCAACCACTCGAATGTGGCTCTGTGCGAGGAGCATGATCATGTGAGGTATCGAC	723		
QY	221	HisSerLeuTyrThrGlySerLeuTrpYrThrProIleArgArgGluTrpYrYrGlu	240		
DB	724	CACCTGCTGTACACGAGCATCTCTGTATACCCCATCCGGGGGAGTGTATTATGAG	783		
QY	241	ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetLysPylGlyGlyTr	260		
DB	784	GTCATCATTTGGGGGTGAGATCATGTGACAGGATCTGAATATGATGACATGCAAGAGTAC	843		
QY	261	AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysLysVal	280		
DB	844	AACATATGACAAAGCATTTGGACATGTGGCACCACTCTGTTGTCCCAAGAAAGTG	903		
QY	281	PheGlnAlaAlaValLysSerIleLysAlaAlaSerSerThrGluLysPheProAspGly	300		
DB	904	TTTGAAGCTGGCATCAATTCATCAAGGACGCTCTCCACGGAGAAATTCCTCATGTGT	963		
QY	301	PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe	320		

Db	964	TTCTGGCTAGAGAGAGACGCTGGTGTGCTGGCAAGACGACCAACCCCTTGGAAACATTTTC	1023
Qy	321	ProVal111SerLeuTyrLeuMetGlyGluVal1ThrAsnGlnSerPheArg111LeThr111	340
Db	1024	CCAGTCATCTCACTTACCTTAATGGGTGAGGTATACCAACGATCTCTCCGATCACCATC	1083
Qy	341	LeuProGlnGluTyrLeuArgProValGluuAspVal1AlaThrSerGlnAspAspCysTyr	360
Db	1084	CTTCGGCACCAATACCTCGCGGCAGAGGAAGATGGGCCACCTCCCAAGACGACTGTTC	1143
Qy	361	LYSPheAla111SerGlnSerSerThrGlyThrValMetGlyAlaVal111LeuMetGluGly	380
Db	1144	AAGTTGGCATCTCAACAGTCATCCACGGGCACATGTTATGGAGCGCTGTATCATGAGAGGC	1203
Qy	381	PheTyrValVal1PheAspArgAlaArgLyAsn111GlyPheAlaVal1Ser1AlaCysHis	400
Db	1204	TTCTACGTTGTCTTGGATGGGCCCGGAACCAATTTGGCTTGTGCTGACGCGCTTGGCAT	1263
Qy	401	Val1H1sAspGluPheArgThrAlaAlaVal1GluGlyProPheVal1ThrLeuAspMetGlu	420
Db	1264	GTGCACGAGATTCACGACGCGCACCGGTGGAGAGCCCTTTTGTGATCCTTGACATGGAA	1323
Qy	421	AspCysGlyTyrAsn111LeuProGlnThrAspGlnSerThr	433
Db	1324	GACTGTGGCTACACATTCACAGACAGATGATCAACC	1362
RESULT 5			
ADL18183	ID	ADL18183 standard; cDNA; 1506 BP.	
XX	AC	ADL18183;	
XX	DT	06-MAY-2004 (first entry)	
XX	DE	Human APP beta-secretase encoding cDNA SEQ ID NO:103.	
XX	KW	chimeric protein; signal protein; trafficking signal targeting;	
XX	KM	proteolytic cleavage site; protease; protease inhibitor; enzyme; human;	
XX	KW	APP beta-secretase; gene; ss.	
OS		Homo sapiens.	
PN		MO2003014381-AL.	
XX	PD	20-FEB-2003.	
XX	PF	08-AUG-2002; 2002WO-KR001515.	
XX	PR	10-AUG-2001; 2001KR-00048123.	
PA		(AHRM-) AHRM BIOSYSTEMS INC.	
XX	PI	Hwang I, Kim DH, Lee YJ;	
XX	PI	WPI; 2003-256596/25.	
XX	DR	P-PSDB; ADL18184.	
XX	PT	New chimeric protein, useful for detecting protease inhibitors inside the	
XX	PT	cell or tissue.	
XX	PS	Disclosure; SEQ ID NO 103; 214pp; English.	
XX	PS	The present invention describes a chimeric protein comprising at least	
XX	CC	one signal protein that has a trafficking signal targeting to a	
XX	CC	subcellular organelle and at least one proteolytic cleavage site for a	
XX	CC	protease. The chimeric protein is constructed, so that: (a) the	
XX	CC	trafficking signals of all the signal proteins are inactivated by linking	
XX	CC	the proteolytic site or a signal masking protein through the proteolytic	
XX	CC	site to the N- or C- terminus of the signal proteins; and so the chimeric	
XX	CC	protein is present in cytosol; (b) the trafficking signal of at least one	
XX	CC	signal protein is activated when the proteolytic cleavage site is cleaved	
XX	CC	by the protease; and as a result at least one fragment protein that	
XX	CC	includes the activated signal protein is a transported to a subcellular	

organelle; and (c) the chimeric protein is labeled with at least one fluorescent protein and the position and intensity distribution of the fluorescent label signal in the cell is altered depending on the cleavage by the protease. Also described: (1) a recombinant gene comprising a nucleic acid sequence encoding the chimeric protein which is constructed to express the chimeric protein in a cell; (2) a cell transformed with the recombinant gene or vector; (3) analysing the activity of a protease *in vivo*; (4) screening protease inhibitors *in vivo*; (5) a system for detecting a protease inside a cell; (6) a nucleic acid comprising the sequence encoding the chimeric protein for detecting protease activity in a cell; (7) a vector comprising the nucleic acid; (8) a kit for detecting a protease inside a cell comprising the chimeric protein or the vector; (9) detecting a protease inside a cell or tissue; and (10) detecting a protease inhibitor *in vivo*. The chimeric protein is useful for detecting protease inhibitors inside the cell or tissue. The present sequence encodes a human APP beta-secretase, which is used in the exemplification of the present invention.

SQ Sequence 1506 BP; 306 A; 449 C; 431 G; 320 T; 0 U; 0 Other;

Alignment Scores:

```

File: NO.: 2.03e-22/ Length: 1506
Score: 2267.00 Matches: 429

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Percent similarity:	99.31%	Conservative:	1
Best local similarity:	99.08%	Mismatches:	3

Query Match:	99.08%	Indels:	0
DR:	10	Calls:	0

NYC 10-722 6673 04 (1 433) -- 10110103 (1 266)

[illegible]

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QUESTION

[illegible]

DD 124 CGGCTGCCCGAGACCGACGAGAGCCCGAGAGCCCGCCCG

QY 41 GIuMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyr

Db 184 GAGATGGTGACAACTGAGGGGCACTCGGGGCAAGGCTACTA

61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySer

Db 244 GGACAGCCCCCGCAGACGCTCAACATCCTGTGGATACAGGCAAG

QY 81 GLYALAALProHisProPheLeuHisArgTyrTyrGlnArgGln

Db
304 GGTGCTGCCCCCAACCCCTTCTGCAATGCTACTTATCCAGAGGCA

101 ArcAsnI,euArctI,vagI]vvaI]TurvaI]ProTvmthncI]ngI]vI,v

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[illegible]

DB 484 GCCATCACTGAAACAGACCAAGTCTCTTCAATCAACGGCTCCAACTGG

161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluIuprc

Db 544 CTGGCCTATGCTGAGATTGCCAGGCTGACGACTCCCTGAGCCT

181 VallysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCys

D5 604 GTAAAGCAGACCCACGTTCCCAACCTCTTCTCCCTGCAGCTTTGT

201 LeuAnGlnSerGluValLeuAlaSerValGlyGlySerMetIle

664 CTCAACCACTCTGAAGTCTGCGCTCTGTGGAGGAGCATGATC

QY 221 HisSerLeuYrThrGlySerLeuTrpYrThrProIleArgGluTrpYrTrpGlu 240
DB CACTGGCTGTACACAGGAGTCTGTGTATACACCATCCGGCGGAGTGGATTATGAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuValMetAspCysLeuGlyTrp 260
DB GTCAATCATGTGCGGGTGAAGATCAATGACAGATCGAATGAAATGACTGACAGAGTAC 843
QY 261 AsnYrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
DB AACTATGACAGAGCATTTGTGACAGTGGACACCACTTCCTTGGCCAGAAAGTG 903
QY 281 PheGluAlaIleValLysSerIleLysValAlaSerSerThrGluLysPheProAspGly 300
DB TTTGAAAGCTGACGTCAAAATCCATCAAGGACAGCTCTCCACGAGAAAGTTCCCTATGAT 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnIleAspYrThrProThrAsnIlePhe 320
DB TTCTGGCTAAGAGACAGCTGGTGTGTGGCAAGGACCACTTGGAAACATTTTC 1023
QY 321 ProValIleSerLeuYrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB CCAATCATCTCACTTAACCTTAATGGGTAGGTTACCAACCACTCTCCGATCACATC 1083
QY 341 LeuProGlnGlnYrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTrp 360
DB CTTCGCGACATATCACTGGCGCCAGTGGAAAGTGTGCCACCTCCAGACACATGTTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyValIleMetGluGly 380
DB AAGTTTGCATCTCAACATCAACATCAACGCGGCTGTTATGGAGCTGTTATCAATGAGGAC 1203
QY 381 PheYrValIleValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
DB TTCTACGTTGTCTTGTGATCGGCGCCGAAACCAATGGCTTGTCTGACGCGCTTGCCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB GTGCAAGATGATTCAGACGCGGACGCGGTGAAGGCCCTTTGTCACTTGGACATGAGAA 1323
QY 421 AspCysGlyYrAsnIleProGlnThrAspGluSerThr 433
DB 1324 GACTGTGGCTACAACTTCACAGACAGATGAGTCAACC 1362

RESULT 6
AD082259
ID AD082259 standard; cDNA; 1524 BP.

AC AD082259;
XX
XX
DT 21-OCT-2004 (first entry)
XX
DE Human BACE1 coding sequence.
XX
XX transgenic animal; beta-site amyloid precursor protein cleaving enzyme;
XX BACE1; Hemostatic; Neuroprotective; Neotropic; Beta-secretase inhibitor;
XX amyloid beta; neurodegenerative disease; Alzheimer's disease;
XX cerebral amyloid angiopathy; Lewy body dementia; Down's syndrome;
XX hereditary cerebral hemorrhage; amyloidosis; Guam Parkinson-Dementia; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX MO2004062627-A2.
XX
XX
XX 29-JUL-2004.
XX
XX 13-JAN-2004; 2004MO-US000883.
XX
XX 13-JAN-2003; 2003US-0439633P.
XX
XX (REGC) UNIV CALIFORNIA.
PA

XX
PI Masliah E, Rockenstein E;
XX
XX WPI; 2004-544036/52.
DR
XX
XX New non-human transgenic animal overexpressing the (human) beta-site
PT amyloid precursor protein cleaving enzyme (BACE1), useful as a model for
PT conditions such as Alzheimer's disease, and in screening for therapeutic
PT agents.
XX
XX Example 1; SEQ ID NO 1; 54pp; English.
XX
XX The present invention relates to a transgenic non-human animal for
CC overexpressing beta-site amyloid precursor protein cleaving enzyme
CC (BACE1) comprising cells containing a DNA transgene encoding for BACE1.
CC The transgenic non-human animal is useful as a disease model, in studying
CC the in vivo and in vitro regulation and effects of BACE1 in specific
CC tissue types, in examining the role of BACE1 proteins in the accumulation
CC of amyloid beta, and for developing therapies for amyloid beta-related
CC conditions. The method, agents or compositions are useful for treating
CC neurodegenerative disease, e.g. Alzheimer's disease, cerebral amyloid
CC angiopathy, Lewy body dementia, Down's syndrome, hereditary cerebral
CC hemorrhage with amyloidosis (Dutch type), or Guam Parkinson-Dementia
CC complex. The present sequence represents human BACE1 coding sequence.
XX
SQ Sequence 1524 BP; 309 A; 456 C; 437 G; 322 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 2,086-227 Length: 1524
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 13 Gaps: 0
US-10-726-967A-84 (1-433) x AD082259 (1-1524)
QY 1 ThrGlnHisGlyTLeuArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB 76 ACCCGACAGGAGATCGGCTGCTGCGCAGCGGCTGGGGGCGCCCCCTGGGGCTG 135
QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGluYrArgArgGlySerPheVal 40
DB CGGCTGCCCCCGGAGACCGAGCAAGAGCCGAGAGCCCGCGGAGGGGAGCTTTGG 195
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyYrYrValGluMetThrVal 60
DB GAGATGGTGGACAACTGAGGGGCAAGTGGGGGAGGCTTACTAGTGAATGACCGTG 255
QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAspPheAlaVal 80
DB GGCAGCCCCCGCACAGCTCAACATCTGTGTGATACAGGACGAGCAATTAATTCAGTG 315
QY 81 GlyAlaAlaProHisProPheLeuHisArgYrYrGlnArgGlnLeuSerSerThrYr 100
DB GGTGTGCCCCCGCACCCCTTCTGTGATGCTTACAGAGGCACTGTCCAGCACATAC 375
QY 101 ArgAspLeuArgLysGlyValYrValProYrThrGlnGlyLysTrpGluGluLeu 120
DB CGGAGCTCCGGAAGGGTGTATGTGCTCTACACCCAGGGGCAAGTGGGAAAGGGAGCTG 435
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
DB GGCACCGACCTGTGTAGCATTCGCCAATGCCCCCAAGTCACTGTGCGTCCAACTGTCT 495
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTrpGluGlyLysLeuGly 160
DB GGCATCACTGAATTCAGACAGATTTCTTCAACAGGCTCCAACTGGGAAGGATCTCTGGG 555
QY 161 LeuAlaYrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB 556 CTGGCTTATGCTGAGATTGCGAGGCTGACGACTCCCTGAGACCTTTCTTACTCTCTG 615

QY 181 VallysglnThrHisValProAsnLeuPheSerLeuGlnLeuCyGlyAlaGlyPhePro 200
DB 616 GTAAAGCAGACCCAGGTTCCAACTCTTCCCTGCGAGCTTGGGCTGCGCTCC 675
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyValAsp 220
DB 676 CTCAACCAAGTCTGAAGTCTGCGCTCTCTCGAGGAGCAAGATCATTTGAGGATGAC 735
QY 221 HisSerLeuYrThrGlySerLeuThrPheProIleArgArgGluValPheVal 240
DB 736 CACTCGCTGACACAGGAGCTCTGTGTATACCCATCCGCGGAGGTGTATTATAG 795
QY 241 ValIleValAlaValGluValGluIleAsnGlyGlnAspLeuMetAspCyGlyVal 260
DB 796 GTGATCATTTGTGGGGTGGAGATCATATGACAGGATCTGAATGACCTGAGAGAGTAC 855
QY 261 AsnTyrAspIysSerIleValAspSerGlyThrThrAsnLeuArgLeuProValVal 280
DB 856 AACTATGACAAAGACATTTGTGACAGTGGCACCAACCTTGCTTGCCCAAGAAAGTG 915
QY 281 PheGluAlaAlaValLysSerIleValAlaSerSerThrGlyLysPheProAspGly 300
DB 916 TTTCAGCTGACAGTCAAAATCATACAGGAGCTCTCCACGAGAAATTCCTGTATGGT 975
QY 301 PheTyrLeuGlyGlnGlnLeuValCyGTrpGlnAlaGlyThrThrProTyrAsnIlePhe 320
DB 976 TTCTGCTAGAGAGCAGCTGTGTGTCTGCAAGAGGACCACTTGTGAAATTTTC 1035
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB 1036 CAGCTACTCTCACTTAACTTAAATGGGTGAGGTATCCAAACAGTCTTCCGATCACATC 1095
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCyGTrp 360
DB 1096 CTTCGGACGAATACCTGGGCGGAGTGGAAAGATGTGGCCACGTCCTCAAGATCGTTAC 1155
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGly 380
DB 1156 AAGTTTGCCATCTCAACAGTATCATCAGGCGACGTGATGAGCTGTATCATGAGAGGC 1215
QY 381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerIleAspHis 400
DB 1216 TTCTAGTTGTCTTATATCGGCGCCCAAAACAAATTTGGCTTGTCTGACGCCCTTGCAT 1275
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1276 GTGCACGATGAGTTCAAGACGGCAGCGGTGGAAGGCCCTTTGTCACTTGGACATGAA 1335
QY 421 AspCyGlyTyrAsnIleProGlnThrAspGluSerThr 433
DB 1336 GACTGTGGCTTCAACATTCACAGACAGATGAGTCAACC 1374

RESULT 7
ABA02406
ID ABA02406 standard; cDNA; 1527 BP.
XX
XX ABA02406;
DT 26-FEB-2002 (first entry)
XX
XX
XX FLAG-tagged human beta-secretase encoding cDNA.
DB Human; beta-secretase; FLAG tag; inhibitor; amine compound;
XX beta amyloid precursor protein production; head injury; spinal injury;
KW amyloid precursor protein secretion; nerve damage;
KW meningitis sequelae; cerebral paralysis; memory disorder; mental disease;
KW neurotropic; neuroprotective; cerebroprotective; ss.
OS Homo sapiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
FT CDS 1..1527

FT /*tag= a
FT /partial
FT /product= "FLAG-tagged human beta-secretase"
FT /note= "No stop codon given in the specification"
XX
XX MO200187293-A1.
XX
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XX 22-NOV-2001.
XX
XX 18-MAY-2001; 2001MO-0P004144.
XX
XX 19-MAY-2000; 20000P-00152758.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Miyamoto M, Matsui J, Fukumoto H, Tani N;
PI
XX
XX MPI; 2002-055640/07.
DR
XX P-PSDB; AM52897.
XX
XX
XX Beta-secretase inhibitor used for treating e.g. Alzheimer's disease and
PT injury to brain or spine, and neurodegeneration, comprises amine
PT compound.
XX
XX
XX Example; Page 78-79; 86pp; Japanese.
XX
XX
XX The invention relates to novel amine compounds which are beta-secretase
CC inhibitors. The beta-secretase compounds also have the ability to promote
CC amyloid precursor protein alpha secretion and to inhibit beta amyloid
CC protein production. The beta-secretase inhibitors of the invention can be
CC used for treating head or spinal injuries, nerve damage, sequelae of
CC meningitis, cerebral paralysis, memory disorders and mental disease. The
CC present sequence represents cDNA encoding a FLAG-tagged human beta-
XX secretase used in the exemplifications of the invention
XX
SQ Sequence 1527 BP; 315 A; 451 C; 438 G; 323 T; 0 U; 0 Other:
XX
XX
XX Alignment Scores:
XX Pred. No.: 2.09e-227 Length: 1527
XX Score: 2267.00 Matches: 429
XX Percent Similarity: 99.31% Conservative: 1
XX Best Local Similarity: 99.08% Mismatches: 3
XX Query Match: 99.08% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-10-726-967a-84 (1-433) x ABA02406 (1-1527)
QY 1 ThrGlnHisGlyTyrLeuArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB 64 ACCCAGACAGGCAATCCGGCTGCGCCCTGCGCAGCGGCTGGGGGGCCCCCTTGGGGCTG 123
QY 21 GlnIleAsnLeuGlnThrAspGluThrArgGluProGluGluPheArgGlySerPheVal 40
DB 124 CGGCTGCCCCGGAGAGCCGACAGAGAGCCCGGAGGCCCGCGAGGGGCGAGCTTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
DB 184 GAGATGTGGACATCTGAGGGCAAGTCGGGGCAAGGCTACTAGTGAAGTGAACCTG 243
QY 61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySerSerAspPheAlaVal 80
DB 244 GGCAGCCCCCCCCACAGCTCAACATCTGGTGATACAGGACAGACATTTGCACTG 303
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
DB 304 GGTGCTGCCCCCACTCCCTTCTGATGCTACTACAGAGGAGGCTGTCCAGACATAC 363
QY 101 ArgAspLeuArgLysGlyValTyrValProTyrThrGlnGlyLysTrpGluGlyValLeu 120
DB 364 CGGAGCTTCGGAGAGGTGTGTATGTGCTTACCCAGGCGCAAGTGGGAAGGGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140

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Db      424 GGCACCGACCTGGTAAGCATCCCCATGGCCCAACCTCATCTGTCGTCGCCAACATTCCT 483
Qy      141 AAlaIeThrgIuSeAspLyBhePheIleAnGIySeRAsnTrpGluGlyIleGluGly 160
Db      484 GCCATCATCATGATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAAGGACATCTCGGG 543
Qy      161 LeuAlaYrAlaGluIleAlaArpProAspAspSerLeuGluProPhePheAspSerLeu 180
Db      544 CTGGCTTATGTGATGATTCGCCAGGCTTCAACCTCCCTGGAGCCCTTCTTGGACTCTCTG 603
Qy      181 VallysGIInThrAlaValProAsnLeuPheSerLeuGluLeuCYsGIYAlaGlyPhePro 200
Db      604 GTPAAGCAAGACCCAGCTTCCCACTCTTCTCCCTGCACTTGTGGTCTGGCTTCCCTCC 663
Qy      201 LeuAnGIInSerGIuValLeuAlaSerValGIyGIySerMetIleIleGIYGIYIleAsp 220
Db      664 CTCAACCAAGTGTGAAGTGTGGCTCTGTGCGAGGAGAGATGATCATGAGAGATTCGAC 723
Qy      221 HisSerLeuYrThrGIySerLeuTrpYrThrProIleArGIuGluTrpYrYrGIu 240
Db      724 CACTCGCTGTACACAGGAGCTCTGTGTATACACCCTCCGGCGGAGTGTATTATGAG 783
Qy      241 ValIleIleValArGIuValGIuIleAnGIyGIuAspLeuMetAspCYsIyAspGIYr 260
Db      784 GTGATCATTTGGCGGATGAGATCATAGGACAGATCTGAAATGACTGCAAGAGATTC 843
Qy      261 AsnYrAspLySerIleValAspSerGIYrThrThrAsnLeuArGIuProIyAsIyVal 280
Db      844 AACTATGACAAAGCATTTGTGACAGTGGCACCAACCACTTCGTTTGGCCAAAGAAAGTG 903
Qy      281 PheGluAlaAlaValIySerIleYValAlaAspSerThrGIuYsPheProAspGIY 300
Db      904 TTTGAAGCTGCGAGTCAATCCATCAAGGACGCTCTCCACGAGAGTTCCTCATGTGT 963
Qy      301 PheTrpLeuGIYGIuGluLeuValCYsTrpGIuAlaGIYThrThrProTrpAsnIlePhe 320
Db      964 TTCTGGCTGAGAGAGAGCTGTGTGTGGCAAGGACCAACCCCTTGGACATTTTC 1023
Qy      321 ProValIleSerLeuYrLeuMetGIYGIuValThrAsnGIuSerPheArGIYIleThrIle 340
Db      1024 CCAAGTCATCTCACTCACTAATGGGTAGGTTACCAACCAAGTCTTCGCAATCACATC 1083
Qy      341 LeuProGIuGIuYrLeuArGIuProValGIuAspValAlaThrSerGIuAspCYrYr 360
Db      1084 CTTCCGCAAGCAATACCTGGCGCAGAGGAAGTGTGCCACGTCCTCAAGACCACTGTATC 1143
Qy      361 LysPheAlaIleSerGIuSerSerThrGIYrThrValMetGIYAlaValIleMetGIuGly 380
Db      1144 AAGTTTGCATCTCAAGTCATCCAGGCGCACTGTATGAGAGCTGTATCATGAGAGGC 1203
Qy      381 PheYrValValPheAspArGIuArGIYsArGIYIleGIYAlaValIleSerAlaCYsHis 400
Db      1204 TTCTAAGTTGTCTTGTGATCGGGCCGCAAAACAAATGGCTTGTCTGTACCGCTTGCAT 1263
Qy      401 ValHisAspGIuPheArGIuThrAlaValGIuGIYProPheValThrLeuAspMetGIu 420
Db      1264 GTGCAAGATGATTCAGACGGGAGGGGTGAAGGCCCTTTGTCTCACTTGACATGAGAA 1323
Qy      421 AspCYsGIYrYrAsnIleProGIuInThrAspGIuSerThr 433
Db      1324 GACTGTGGCTACAAACATTCACAGACAGATGATCAACC 1362

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RESULT 8
ADJ71857
ID ADJ71857 standard; cDNA; 1527 BP.
XX
XX ADJ71857;
XX
XX 06-MAY-2004 (first entry)
XX
XX Human cDNA SEQ ID NO: 6.
XX
XX N-Substituted aryl carboxamide; neuroprotective; nootropic; neuroleptic;

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KW muscular; antiparkinsonian; cerebroprotective; vasotropic; haemostatic;
KW antidiabetic; antidiabetic; antidepressant; neurodegeneration; nerve damage;
KW memory disorders; psychiatric disease; myopathy;
KW mild cognitive impairment; Alzheimer's disease; ss; gene; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1527
FT /*tag= a
PD MO2004014843-A1.
PD 19-FEB-2004.
PF 07-AUG-2003; 2003WO-JP010045.
PR 09-AUG-2002; 2002JP-00233231.
PR (TAKE ) TAKEDA CHEM IND LTD.
PI Uchikawa O, Aso K, Kolke T, Tani N, Hirai K;
PI WPI; 2004-238691/22.
DR P-PSDB; ADJ71858.
XX
XX New/known aryl carboxamide derivatives as inhibitors of aspartic acid
XX protease and beta secretase for treating Alzheimer's disease.
XX neurodegeneration, nerve damage, memory disorders, psychiatric disease,
XX myopathy and cognitive impairment.
XX
XX Example 1; SEQ ID NO 6; 90pp; Japanese.
XX
XX The invention relates to novel N-Substituted aryl carboxamide compounds
XX (I) and their salts. A compound of the invention has neuroprotective,
XX nootropic, neuroleptic, muscular-gen., antiparkinsonian,
XX cerebroprotective, vasotropic, haemostatic, antidiabetic, antidiabetic, and
XX antidepressant activity. The compounds are used to prevent and treat
XX neurodegeneration, nerve damage, memory disorders, psychiatric disease,
XX myopathy, mild cognitive impairment, or Alzheimer's disease, including
XX Down's syndrome, senile dementia, Parkinson's disease, Creutzfeldt-Jacob
XX disease, amyotrophic lateral sclerosis, diabetic neuropathy, Huntington's
XX chorea, multiple sclerosis, cerebrovascular disorders, cerebral embolism,
XX cerebral haemorrhage, cerebral arteriosclerosis, head injuries, spinal
XX cord injuries, post-encephalitic disease, cerebral palsy, depression, panic
XX disorder and schizophrenia. The present sequence is used in the
XX exemplification of the invention.
SQ Sequence 1527 BP; 317 A; 447 C; 438 G; 325 T; 0 U; 0 Other;

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Alignment Scores:
Pred. No.: 2,096-227 Length: 1527
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conserved: 1
Best Local Similarity: 98.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 12 Gaps: 0
US-10-726-967a-84 (1-433) x ADJ71857 (1-1527)
Qy      1 ThrGlnHisGIYIleArGIuProLeuArGIYIleGluYAlaProLeuGIYLeu 20
Db      64 ACCCAGCAGCGGATCCGCTGCTGAGAGATGTGTGGGGGGGCCCCCTGGGGCTG 123
Qy      21 GluIleAsnLeuGIuThrAspGIuGIuProGIuGIuProGIYArGIYArGIYSerPheVal 40
Db      124 CGGCTGCCCGGGGAGACGAGCAAGAGGCCGAGGACCCGCGGAGGGGAGCTTTGG 183
Qy      41 GluMetValAspAsnLeuArGIYIySerGIYGIuGIYIleGIYIleValGluMetThrVal 60
Db      184 GAGATGTGTGACCAACTGAGGCGCAAGTGTGGGCGAGGCTACTTACGTGAGATGACCGTG 243
Qy      61 GlySerProProGIuInThrLeuAsnIleLeuValAspThrGIYSerSerAsnPheAlaVal 80

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Db      244  GGCAGCCCCCGCAGAGCTCAACATCTGATGATACAGCAGACGACTTTCGACTG 303
Qy      81  GLVLAALAPROHLEPProPheLeuHISArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db      304  GGTGTGCCCCCACCCTTCTGCTGATGCTTACACAGAGGAGCTGTCCAGACATAC 363
Qy      101  ArgAPLeuAArgLysGlyValTyrValProTyrThrGlnGlyLysTPGInGlnLeu 120
Db      364  CGGACCTCCGGAGGGGTGTATGTGCTTACACCGAGGAGGAGGAGGAGGAGCTG 423
Qy      121  GlyThrAPLeuValSerLeProHISGlyProAenValThrValArgAlaAenLea 140
Db      424  GGCACCGCCTGTGTACATCCCATGCGCCCAACGTCAGTGGCTGCACATTCGCT 483
Qy      141  AlAlLeThrGlnSerAPLeuPhePheHISLeuGlySerAenTPGInGlyLysLeu 160
Db      484  GCCATCTGATATGACCAAGTCTTCATCAACGGCTCCAACTGGGAGGCATCTGGGG 543
Qy      161  LeuAlaTyrAlaGlnIleAlaArgProAPLeuSerLeuGlnProPheAPLeu 180
Db      544  CTGGCTATGTGTAGATTGCTGACGGCTGACGACTCCCTGAGCTTCTTGACTCTG 603
Qy      181  ValLysGlnThrHISValProAenLeuPheSerLeuGlnLeuCysGlyAlaGlyPhePro 200
Db      604  GTAAAGCAGACCCAGTTCCTCCACTCTCCCTGAGCTTGTGGTGGCTTCCCTCC 663
Qy      201  LeuAenGlnSerGlnValLeuAlaSerValGlyLysSerLeuIleLysGlyLysLeu 220
Db      664  CTCACACAGCTGTAAGTGTGGCTCTGTGAGAGGAGCATGATGATGAGATTCGAC 723
Qy      221  HISSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgLysTyrTyrGln 240
Db      724  CACTCGCTGTACACAGGCACTCTGGTATACACCATCGGGAGGTGATTTATGAG 783
Qy      241  ValIleLysValArgValGlnIleAenGlyGlnAPLeuLysMetAPCysLysGlyTyr 260
Db      784  GTATCATGTGTGGGGTGAGATCAATGACAGATCTGAAATGATGACGCAAGAGTAC 843
Qy      261  AenTyrAPLeuSerLeuIleValAPSerGlyTyrThrAPLeuArgLeuProLysLysVal 280
Db      844  AACTATGACAGAGCATGTGTGACATGTCGACACCAACCTTCGTTGCTCCAGAAAGTG 903
Qy      281  PheGlnAlaAlaValLysSerIleLysValAlaIleSerSerThrGlnLysPheProAPGly 300
Db      904  TTTGAAGCTGCAGTCAATTCATCAAGCAGCTCTCCACGAGAAAGTTCCCTGATGCT 963
Qy      301  PheTPLeuGlyGlnGlnLeuValCysTPGInAlaGlyTyrThrProTPAenIlePhe 320
Db      964  TTTGCTGTGAGAGAGCATGTGTGTGCTGCAAGCAGGACCACTTGGAAACATTTTTC 1023
Qy      321  ProValIleSerLeuTyrLeuMetGlyGlnValIleAenGlnSerPheArgIleThrIle 340
Db      1024  CCAGTCATCTCACTCACTAATGGGTGAGTTACCAACCACTCTTCGATCCATCCATC 1083
Qy      341  LeuProGlnGlnTyrLeuArgProValGlnAPValAlaIleThrSerGlnAPLeuPheCysTyr 360
Db      1084  CTTCCGAGCAATACCTGGGCGAGTGAAGATGTGGCCACCTCCCAAGACGACTGTAC 1143
Qy      361  LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGlnGly 380
Db      1144  AAGTTTGCATCTCAAGTCAATCCACGGGCACTGTTATGGAGCGTATATATGAGAGGC 1203
Qy      381  PheTyrValValPheAPArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHIS 400
Db      1204  TTTCTAGTTGCTTGTGATGCGGCGGAAACGAATGTGCTTGTGCTGCAAGGCTTGCAT 1263
Qy      401  ValHISAPBGInuPheArgThrAlaAlaValGlnGlyProPheValThrLeuAPMetGln 420
Db      1264  GTGCGAGATGAGTATGAGACGGCAGCGGTGAGAGGCCCTTTGTGTCACTTGAGACATGGA 1323
Qy      421  APGcysGlyTyrAenIleProGlnThrAPGlnSerThr 433

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Db      1324  GACTGTGCTACACATTCACAGACAGATGATGACACC 1362
RESULT 9
ADP74534
ID      ADP74534 standard; cDNA; 1527 BP.
XX
AC      ADP74534;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Human indole compound-related beta-secretase cDNA.
XX
KW      indole; neuroprotective; nootropic; antiparkinsonian; myopathy;
KW      neuropathy; memory defect; senile dementia; amnesia; mental illness;
KW      neurodegenerative disease; Alzheimer's; Creutzfeldt Jacob; CJD;
KW      amyotrophic lateral sclerosis; Parkinson's; beta-secretase; ss; gene;
KW      human.
XX
OS      Homo sapiens.
XX
FH      Key
FT      Location/Qualifiers
FT      CDS
FT      1..1527
FT      /tag= a
FT      /product= "Human indole compound-related beta-secretase
FT      protein"
PN      JP2004149429-A.
XX
PD      27-MAY-2004.
XX
PF      29-OCT-2002; 2002JP-00314580.
XX
PR      29-OCT-2002; 2002JP-00314580.
XX
PA      (TAKE ) TAKEDA CHEM IND LTD.
XX
DR      WPI; 2004-405630/38.
XX
DR      P-PSDB; ADP74535.
XX
PT      Novel indole compound useful for treating senile dementia, Alzheimer's
PT      disease, Creutzfeld-Jakob disease, amyotrophic lateral sclerosis,
PT      Parkinson's disease, neuropathy, senile dementia, amnesia or myopathy.
XX
PS      Example 119; SEQ ID NO 6; 67pp; Japanese.
XX
CC      The invention relates to a novel indole compound. The compound of the
CC      invention demonstrates neuroprotective, nootropic and antiparkinsonian
CC      activities and may be useful as a preventive or therapeutic agent of
CC      myopathy, neuropathy, defects of memory e.g. senile dementia or amnesia,
CC      mental illness and neurodegenerative disease, including Alzheimer's
CC      disease, Creutzfeld Jacob disease, amyotrophic lateral sclerosis or
CC      Parkinson's disease. The peptide of the invention may be useful for
CC      measuring the beta-secretase inhibitory activity of a test compound. The
CC      current sequence is that of the human indole compound-related beta-
CC      secretase cDNA of the invention.
XX
SQ      Sequence 1527 BP; 317 A; 447 C; 438 G; 325 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      2,09e-227      Length:      1527
Score:          2267.00      Matches:      429
Percent Similarity: 99.31%      Conservative: 1
Best Local Similarity: 99.08%      Mismatches: 3
Query Match:      99.08%      Indels:      0
DB:              12      Gaps:      0

US-10-726-967A-84 (1-433) x ADP74534 (1-1527)
Qy      1  ThrGlnHISGlyLysArgLeuProLeuArgSerGlyLysGlyValAlaProLeuGlnTyrLeu 20
Db      64  ACCGACAGCAGCATCCGCTGCCCTTGAGAACTGTGTGGGGGCGCCCCCTGTGGGGCTG 123
Qy      21  GlnIleAenLeuGlnThrAPGlnGlnTPGInGlnProGlyArgArgLysSerPheVal 40

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Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 12 Gaps: 0
 US-10-726-967a-84 (1-433) x ADH34044 (1-1542)

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QY 1 ThrGlnHISGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB ACCGAGCAGCGGCACTCCGACTCCGACTGGCAGCGGACTGGAGGATGCACTCGGAGCTG 138
QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
DB CGGTCGCCCCGGGAGACCGAGAGAGCCCGGAGGCGGCGGAGGGGAGCTTTGTG 198
QY 41 GluMetValAspAsnLeuArgGlyLeuSerGlyValGlnGlyTyrValGluMetThrVal 60
DB GAGATGTGGACCACTGAGGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 258
QY 61 GlySerProGlnThrLeuAsnIleValAlaAspThrGlySerSerAspAsnAlaVal 80
DB GGCAGCCCCCGCAGACGCTCAATCATCTGGTGAATACAGGAGAGGAGGAGGAGGAGGAG 318
QY 81 GlyAlaAlaProHISProPheLeuHISArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
DB GGTCTGCCCCCGCAGCCCCCTTCTGCACTGCTACTACAGGAGGAGGAGGAGGAGGAGGAG 378
QY 101 ArgAspLeuArgGlyValTyrValProTyrThrGlnGlyValTyrProGluGluLeu 120
DB CGGAGCTCCGGAAGGAGTGTATGTGCTTACACCCAGGAGGAGGAGGAGGAGGAGGAGGAG 438
QY 121 GlyThrAspLeuValSerIleProHISGlyProAsnValThrValArgAlaAsnIleAla 140
DB GGCAGCCAGCTGTGATGATCATCCCCCAGTGGCCCAAGCTGCTGTGCTGCTCAACATGCT 498
QY 141 AlaIleThrGluSerAspLeuPhePheIleAsnGlySerAspThrGluGlyIleGluGly 160
DB GCCATCACTGATCAACAGAGGATTTCTTCAATCAAGGCTCCCAAGGAGGAGGAGGAGGAG 558
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB CTGGCTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 618
QY 181 ValIleGlnThrHISValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
DB GTRAAACAGACCACTCCCAACTCTTCTCTCCGCACTTGTGCTGCTGCTGCTGCTGCTGCT 678
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleGlyGlyIleAsp 220
DB CTCAACCACTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 738
QY 221 HISerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
DB CACTGCTGTATACAGGAGGAGTCTGTGTATACACCACTCCGCGGAGGAGGATTAATGAG 798
QY 241 ValIleIleValArgValGluIleAsnGlyIleAspLeuValMetAspCysGlyGluTyr 260
DB GTGATCATTTGCTGGGTGAGATCAATGACAGGATCTGAAATGAGACTGCAAGAGATAC 858
QY 261 AsnTyrAspLeuSerIleValAspSerGlyThrThrAsnLeuArgLeuProGlyLeuVal 280
DB AACTATGACAGAGCAATGTGAGCAGTGGCACCAACCACTTCGTTGTTCCCAAGAAAGTG 918
QY 281 PheGluAlaAlaValLeuSerIleValAlaAspSerThrGluValPheProAspGly 300
DB TTTGAAGCTGAGTAAATTCATCAAGGAGCTTCTTCAAGGAGGAGGAGGAGGAGGAGGAG 978
QY 301 PheTyrLeuGlyGluGlnLeuValCysTyrProGlnAlaGlyThrTyrProTyrAsnIlePhe 320
DB TTCTGGCTAGGAGAGCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1038
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB CGAGTCATCTCACTTACTTAATGGGTGAGGTTCACCAACAGTCTCTCCGATCATCATC 1098

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QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
DB CTTCCGAGCAATATCTCTGCGGCACTGCAAGATGTGGCCAGCTCCCAAGAGCACTGTAC 1158
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
DB AGTTTGCATCTTCACATCATCCACGCGCACTGTTATGAGAGCTGTTATCATCATGAGGCG 1218
QY 381 PheTyrValIlePheAspArgAlaArgLysArgIleGlyPheAlaValIleSerAlaCysHis 400
DB TTCTACGTTGCTTTGATTCGAGCCCGGAAACGAATGTGCTTGTCTGTCAGCGCTTGTCCAT 1278
QY 401 ValHisAspGluPheArgThrAlaAlaValGluIleProPheValThrLeuAspMetGlu 420
DB GTGACGATGATGATTCAGGAGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1338
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
DB 1339 GACTGTGCTTCAACATTCACAGACAGATGATCAACC 1377

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RESULT 11

ADJ94315
 ID ADJ94315 standard; cDNA; 2070 BP.

ADJ94315;

03-JUN-2004 (first entry)

Human cDNA encoding aspartyl protease 2a, Asp-2a.

Human; ss; gene; aspartyl protease; Asp-1; Asp-2(a); Asp-2(b);
 beta secretase; amyloid protein precursor; APP; Alzheimer's disease;
 neurotic; neuroprotective; amyloid beta.

Homo sapiens.

US6706485-B1.

16-MAR-2004.

12-APR-2000; 2000US-00548376.

24-SEP-1998; 98US-0101594P.

23-SEP-1999; 99US-00404133.

23-SEP-1999; 99US-0155493P.

23-SEP-1999; 99WO-US020881.

13-OCT-1999; 99US-00416901.

(PMDA) PHARMACIA & UPJOHN CO.

Gurney ME, Bienkowski MJ, Heinrikson RL, Parodi LA, Yan R;

WPI; 2004-236722/22.

P-PSDB; ADJ94316.

Identifying agents that modulate activity of Asp2 aspartyl protease

useful for treating or preventing Alzheimer's disease involves comparing

APP processing activity of protease in presence and absence of test

agent.

Example 2; SEQ ID NO 3; 109bp; English.

The invention relates to identifying agents that modulate activity of
 Asp2 (e.g. a beta-secretase, e.g. human Asp-2(b) appearing as ID 6,
 encoded by ID 5) aspartyl protease, involves contacting Asp2 with amyloid
 precursor protein (APP) in the presence and absence of a test agent,
 where Asp2 is a recombinant polypeptide and processes APP into amyloid
 beta, determining APP processing activity of Asp2 in presence and absence
 of the test agent, and comparing the activities to identify agents that
 modulate the activity of Asp2. Also disclosed are the cDNA and proteins
 for human Asp-1 and Asp-2(a), mouse Asp-2(b), a vector comprising the
 nucleic acid encoding hu-Asp2 protease sequence, a host cell comprising

the vector and the method of producing Hu-Asp polypeptide, an isolated antibody that specifically binds to Hu-Asp polypeptides, identifying a cell that can be used to screen for inhibitors of beta secretase activity, novel isoforms of amyloid protein precursor (APP), where the last 2 carboxy terminus amino acids of that isoform are both lysine residues (e.g. those designated APP695-KK or carrying the Swedish mutation where Km at 595-596 is mutated to NL, designated e.g. APP695-SW or APP695-SW-KK, or a V to F mutation at 642, e.g. APP695-VF, all useful for assaying for beta secretase activity and screening for inhibitors of beta-secretase) and polynucleotides that encode the APP protein. The method is useful for identifying agents that modulate the activity (amyloid precursor protein processing activity) of Asp2 aspartyl protease. Preferably, the method is useful for identifying agents that inhibit Asp2 aspartyl protease activity. The inhibitors of amyloid precursor protein processing, are useful for treating or preventing Alzheimer's disease. The present sequence encodes an aspartyl protease of the invention.

Sequence 2070 BP; 476 A; 582 C; 563 G; 449 T; 0 U; 0 Other;

Alignment Scores:

Score: 3, 21e-227 Length: 2070
 Percent Similarity: 2267.00 Matches: 429
 Best Local Similarity: 99.31% Conservative: 1
 Query Match: 99.08% Mismatches: 3
 Indels: 0
 Gaps: 0

US-10-726-967a-84 (1-433) x ADJ94315 (1-2070)

1 ThrGlnHleGlyIleArgLeuProIleuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
 64 ACCCGACAGCGGATCGGCTGCGCCGCGAGCGGCTGGGGGCGCCCTGGGGCGTG 123
 21 GluIleAsnLeuGlnThrAspGluGluProGluGluPheGlyArgArgGlySerPheVal 40
 124 CGGCTGCGCCGGGAGAGCCAGAGAGCGGAGAGAGCCGGCCGAGGGGCGAGCTTTG 183
 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyIleTyrtValGluMetThrVal 60
 184 GAGATGCTGACACACTGAGGGGCGAGCTGGGGCGAGGGCTACACGTGAGATGACCG 243
 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
 244 GCGAGCGCCCGCAGAGCGCTCAACATCTGCTGATACAGCGCGAGCTTTCAGATG 303
 81 GlyAlaAlaProHisAspPheLeuHisArgTyrtValThrGlnArgGlnLeuSerSerThrTy 100
 304 GGTGCTGCGCCCGACCCCTTCTGCTGATCGCTACTACAGAGGCGAGCTGTCAGACATAC 363
 101 ArgAspLeuArgGlyValTyrtValProTyrtThrGlnGlyLysTrpGluGluLeu 120
 364 CGGAGCTCGGAGAGGCTGTATGCTGCTTACACCCAGGCGAAGGGAGGGAGCGT 423
 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
 424 GGGACCGACCTGGTATGATCCCGCATGGGCCCAAGCTCATGTGCTGCTGCAACATTTG 483
 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160
 484 GGCATCATGAAATCAAGCAAGTTCTTCTATCAACAGGCTCCAACTGGAGGACATCTGGG 543
 161 LeuAlaTyrtAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
 544 CTGGCTTATGCTAGATGCGACAGCTGACGATCTCTTGAAGCTTCTTGAATCTCTG 603
 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyGlyAlaGlyPhePro 200
 604 GTAAACAGACCCACGTTCCCAACCTTCTCCCTGAGCTTGTGTGTGCTGGCTTCC 663
 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerSerIleIleGlyGlyIleAsp 220
 664 CTCACCAAGCTGAGAGTGTGCTCTGTGAGAGGAGCATGATCATTTGAGGATTCGAC 723

221 HisSerLeuTyrtThrGlySerLeuTrpThrProIleArgArgGluTrpTyrtGly 240
 724 CACTGCGTACACAGGAGGCTCTGTATACACCATCCGCGGAGTGTATATAG 783
 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysAlaGlyTy 260
 784 GTCAATCATGTGCGGGTGGATCAATGACAGGATTCGAAATGACATCGAAGAGATAC 843
 261 AsnTyrtAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysPheVal 280
 844 AACTATGACAGAGATGTGACAGTGGCACACCACTTCCTTTCGCCAAGAAATG 903
 281 PheGluAlaAlaValIleValSerIleValAlaIleSerSerThrGluLysPheProAspGly 300
 904 TTGAGAGCTGACGTAAATTCATCAAGGAGCTCTCTTCCAGAGAAATTCCTGATG 963
 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
 964 TTCTGGCTAGAGAGACACTGTGTGCTGGCAGAGGACACACCTTGGAACTTTTC 1023
 321 ProValIleSerLeuTyrtLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
 1024 CCAATCATCTACCTTACCTAATGGGTGAGGTACCAACAGTCTTCCTCCGATCACCATC 1083
 341 LeuProGlnGlnTyrtLeuArgProValGluIleAspValAlaThrSerGlnAspAspCysTy 360
 1084 CTTCGCGAGCAATACCTCGGCGAGTGAAGATGGGCGACGCTCCACAGACGACTTTAC 1143
 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGlyGly 380
 1144 AGTTTGCATCTTCAAGTATCCACGGGCACTGTATGGAGCGTATATCATGAGGGCG 1203
 381 PheTyrtValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
 1204 TTCTACGTTGCTTGTATCGGGCCGAAACGAATGGCTTTGCTGTCAGCGCTTGCCAT 1263
 401 ValIleAspGlnPheArgThrAlaAlaGluGlyProPheValThrLeuAspMetGly 420
 1264 GTGACAGATGATTCAGAGCGGAGCGGTGGAGGCCCTTTGTGCACTTGACATGGAA 1323
 421 AspCysGlyTyrtAsnIleProGlnThrAspGlnSerThr 433
 1324 GACTGTGCTTACATTCACAGACAGATGATGTAACC 1362

RESULT 12
 ADOS0411
 ID ADOS0411 standard; cDNA; 2070 BP.
 XX AC
 XX ADOS0411;
 XX AC
 XX 29-JUL-2004 (fixet entry)
 XX AC
 XX DE Human aspartyl protease (Asp)-2(a) cDNA.
 XX AC
 XX KW Aspartyl protease; Asp; beta secretase; amyloid precursor protein; APP;
 XX KW Alzheimer's disease; gene therapy; human; gene; chromosome 11q23.3-24.1;
 XX ss.
 XX AC
 XX OS Homo sapiens.
 XX AC
 XX Key Location/Qualifiers
 XX FT 1..1506
 XX FT /*tag= b
 XX FT /product= "Human Asp-2 protein"
 XX FT sig_peptide 1..63
 XX FT /*tag= a
 XX FT mat_peptide 64..1503
 XX FT /*tag= c
 XX FT /product= "Human mature Asp-2 protein"
 XX AC
 XX PN US6737510-B1.

PD		18-MAY--2004.	
PF		12-APR-2000; 2000US-00548373.	
XX			
PR	24-SEP-1998;	98US-0101594P.	
XX			
PR	23-SEP-1999;	99US-00404133.	
XX			
PR	23-SEP-1999;	99US-0155493P.	
XX			
PR	23-SEP-1999;	99WO-USO20681.	
XX			
PR	13-OCT-1999;	99US-00416901.	
XX			
PA	(PHNA) PHARMACIA & UPJOHN CO.		
PI	Gurney ME, Bienkowski MJ, Heinriksen RL, Parodi LA, Yan R,		
XX			
DR	WPI; 2004-387112/36.		
XX	P-P8DB; ADO50412.		
XX			
PT	New Asp2 aspartyl protease protein comprising tripeptides DTG and DSG		
PT	involved in processing amyloid precursor protein into amyloid beta.		
PT	useful in preparing a composition for treating or preventing Alzheimer's		
XX	disease.		
PS	Example 2; SEQ ID NO 3; 108bp; English.		
CC	The invention relates to a method for identifying an agent that decreases		
CC	the protease activity of the aspartyl protease (Asp) polypeptide. It also		
CC	provides enzyme and enzymatic procedures for cleaving the beta secretase		
CC	cleavage site of the amyloid precursor protein (APP). The invention is		
CC	useful in preparing a composition for treating or preventing Alzheimer's		
CC	disease. It is also useful in gene therapy. The present sequence is human		
CC	Asp-2 cDNA. Human Asp-2 gene is located at chromosome 11q23.3-24.1. This		
XX	sequence is used to illustrate the method of the invention.		
XX			
SQ	Sequence 2070 BP; 476 A; 582 C; 563 G; 449 T; 0 U; 0 Other;		
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	Pred. No.: 3,21e-227 Length: 2070		
	Score: 2267.00 Matches: 429		
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	Best Local Similarity: 99.08% Mismatches: 3		
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	DB: 12 Gaps: 0		
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OY	21 GluILEaMLeuGlunThraSpJugluPProJugluPProJLyaTgaTGlySerPheVal 40		
Db	124 CGGCTGCCCGGGAGACCGACGAAGAAGCCCGAGAGCCCGGCGAGGGCGACTTTGTG 183		
OY	41 GluMetValaLapMaLeuArgLylysSerGlynglyTYrTyValGluMetThrVal 60		
Db	184 GAATGATGTGACAACCTGAGGGGCAAAAGTCGGGGCGGGCTCTACGTGAGATGACCCTG 243		
OY	61 GlySerProProglunThraLeuanlileuValaLapThrnglylsarsarLanpheAlaVal 80		
Db	244 GGAGACCCCGCGACGCTCAACATCCTGGTGAATACAGGACACAGTAATTGGCACTG 303		
OY	81 GlyAlaLaProHlaProHelaLeuhIsaGrTYrTyrgLnAtgLnLeuSerSerThrTYr 100		
Db	304 GGtGtGtCCCCCACCCCTTCTGTGATGGTACTACAGAGGACGCTGTCCAAGCATAC 363		
OY	101 ArgAspLeuArgLySglyValTyTyValProTYrThrGlnGlylybTPdJugluGlyLeu 120		
Db	364 CGGGAAGCTCGGAAGGGTGTGTATGTGCTTACACCCAGGGCAAGTGGAAAGGGAGCTG 423		
OY	121 GlyThrAspLeuValserIleProHlaIleProHlaGlyProaAnValThrValArgAlaaniLea 140		
Db	424 GGACCGACCTGTGTAGCATCCCCCAAGGCCCAAGCATGAGCTGTGCTGTGCACATTGGCT 483		

QY	141	AlaIleThrGluSerAspIysPhePheIleValGlnGlySerAsnTrpGluIylIleuGly	160
Db	484	GCCATCATCGAATTCAGACAAAGTTCTTATCAACCGCTCCAACTGGGAAGGCATCTGGGG	543
QY	161	IleuAlaIyValaGluIleAlaArgProAspAspSerIleuGluProPhePheAspSerIleu	180
Db	544	CTGGCCCTATGCTGAGATTGCTCCAGGCTGACGATCCCTGGAGCCTTTCTTTGACTCTGTG	603
QY	181	ValIysArgInThHisValProAsnIleuPheSerIleuGlnIleuCyGlyValaGlyPhePro	200
Db	604	GTAAGACAGACCACGATTCACCAACTCTTCTCCCTGGACGCTTGTGGTGTGCTGCTTCC	663
QY	201	IleuAsnGlnSerGluValIleuAlaSerValGlyGlySerMetIleIleGlyIylIleAsp	220
Db	664	CTCAACCAAGTCGAAGTGCTGGCCCTGTCGGAGGAGCATATCATTTGAGAGTATCGAC	723
QY	221	HisSerIleuYrThGlySerIleuTrpYrThrProIleArgArgGluTrpYrYrGlu	240
Db	724	CACCTGCGTGTACACAGGACAGTCTCTGGTATACACCATCCGCGGAGAGTGATTAATGAG	783
QY	241	ValIleIleValaArgValaGluIleAsnGlyGlnAspIleuIysMetAspCyIysArgIuYr	260
Db	784	GTCATCATTTGTGCGGGTGGAGATCATATGACAGGAATCTGAATATGACTGCAAGAGTAC	843
QY	261	AsnYrAspIysSerIleValaAspSerGlyThrTrpAsnIleuArgIleuProIylAsVal	280
Db	844	AACTATGTACAAGAGCATTTGTGACAGTGGCACCAACCACTTCGTTGGCCCAAGAAAGTG	903
QY	281	PheGluAlaAlaValIysSerIleValaIalaSerSerTrpGluIylPheProAspGly	300
Db	904	TTTGAAAGCTGACGTCAAAATCCATCAAGGACAGCTCTCCACAGGAAGATTCCTGATGGT	963
QY	301	PheTrpIleuGlyGluGlnIleuValCyserTrpGlnaIagIylThrProTrpAsnIlePhe	320
Db	964	TTCTGGCTTAGAGAGACAGCTGGTGTGTGGCAGACGACACACCCCTTGGAAACTTTTC	1023
QY	321	ProValIleSerIleuYrIleuMetGlyGluValThrAsnGlnSerPheArgIleThrIle	340
Db	1024	CCAGTCATCTCACTCACTAATGGGTAGGTTTCCAAACCAAGCTCTCCGATCCACATC	1083
QY	341	IleuProGlnGlnYrIleuArgProValaGluAspValaIaThrSerGlnAspAspCyserYr	360
Db	1084	CTTCGCGACGATACCTCGCGGCGGAGTGAATGTGGCCACGCTCCCAAGACGACTGTAC	1144
QY	361	IysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly	380
Db	1144	AAAGTTTGGCATCTCAAGTCATCCACGGGCACTGTTATGGAGCTGTATCATGAGGGC	1203
QY	381	PheTrpYrValValaPheAspArgAlaArgIylArgIyleGlyPheAlaValaSerAlaCyHis	400
Db	1204	TTCTACGTTGCTTTTGTGATCGGAGCCCAAAAGAAATGGCTTGTGCTGCACGGCTTGCAT	1263
QY	401	ValHisAspGluPheArgThrAlaAlaValaGluGlyProPheValThrIleuAspMetGlu	420
Db	1264	GTGACGAGTAGTTCAGAGACGGGACGGGTGGAAGGCCCTTTTGTGCACCTTGACATGGA	1323
QY	421	AspCyArgIylYrAsnIleProGlnThAspGlnSerThr	433
Db	1324	GACTGTGGCTACCAACATTCACACAGACGATGATCAACC	1362
RESULT 13			
ID	ADR75324	standard; cDNA; 2070 BP.	
XX	ADR75324;		
XX	18-NOV-2004	(first entry)	
DE	Human aspartyl protease (Asp-2(a)) cDNA.		
XX	Aspartyl protease; Asp; amyloid precursor protein; APP; amyloid beta;		
XX	chromosome identification; Alzheimer's disease; human; gene; 89.		

QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
|||
Db 1264 GTGCACGATGAGTTAGACGGCAGCGGTGAAGGCCCTTTGTCCACCTGGACATGAA 1323
QY 421 AepCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
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Db 1324 GACTGTGGCTACACATTTCCACAGACATGAGTCAACC 1362
RESULT 14
AAAS9551
ID AAAS9551 standard; DNA; 2348 BP.
XX
XX AC AAAS9551;
XX
XX 14-NOV-2000 (first entry)
XX
XX DNA encoding a human beta-secretase enzyme.
XX
XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KM amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
KM inhibitor; ss.
XX
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 306..1811
FT /*tag= a
FT /product= "beta-secretase"
XX
XX MO200047618-A2.
XX
XX 17-AUG-2000.
XX
XX PF 10-FEB-2000; 2000MO-US003819.
XX
XX PR 10-FEB-1999; 99US-0119571P.
XX PR 15-JUN-1999; 99US-0139172P.
XX
XX PA (ELAN) ELAN PHARM INC.
XX
XX PI Anderson JP, Baal G, Doane MT, Frigon N, John V, Power M;
PI Simha S, Tatsuno G, Tung J, Wang S, Mcconlogue L;
XX
XX DR WPI: 2000-533011/48.
XX
XX DR P-PSDB; AAB07896.
XX
XX PT Purified beta-secretase protein used in assays to discover inhibitors
XX PT which can be used for the treatment of amyloidogenic diseases e.g.
XX PT Alzheimer's disease.
XX
XX PS Disclosure; Fig 1B; 121pp; English.
XX
XX CC The specification describes a beta-secretase enzyme. The enzyme cleaves
XX CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
XX CC enzyme is therefore implicated in the production of amyloid plaque
XX CC components which accumulate in the brains of individuals afflicted with
XX CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
XX CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
XX CC like pathology to test if they maintain or improve cognitive ability or
XX CC reduce the plaque burden. The compounds are used for the treatment of
XX CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
XX CC encodes a human beta-secretase enzyme
XX
SQ Sequence 2348 BP; 489 A; 713 C; 661 G; 484 T; 0 U; 1 Other;

US-10-726-967a-84 (1-433) x AAAS9551 (1-2348)
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QY 21 GluIleAsnLeuGluThrAspGluGluProGluIleProGluIleArgGlySerPheVal 40
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Db 429 CGGCTGCCCGGAGACCGACGAGAGAGCCGAGAGCCCGGCGAGGGGCACTTTGTG 488
QY 41 GluMetValAspAsnLeuArgGlyLeuSerGlyGlnGlyTyrTyrValGluMetThrVal 60
|||
Db 489 GAGATGGTGAACAACCTGAGGGGCAAGTGGGGGCAAGGCTACTACGTGAGATGACCGTG 548
QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
|||
Db 549 GGCAGCCCCCGCAGAGCGTCCACATCTGGTGGATACAGGCAGACATTACTTTGCAAGT 608
QY 81 GluValAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
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Db 609 GGTCTGCCCCCACCCTTCTGCTGCTACTACAGAGGCAAGCTGTCCAGCACTAC 668
QY 101 ArgAspLeuArgGlyGlyValTyrValProTyrThrGlnGlyTyrGluGlyLeu 120
|||
Db 669 CGGACCTCCGGAGAGGGTGTATGTGCCCTACACCCAGGCGCAAGTGGAAAGGGAGCTG 728
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValAlaAsnIleAla 140
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Db 729 GGCACCCACCTGGTACACATCCCCCATGGCCCCCAACCTCACTGGCCGTGCCAACATTTGCT 788
QY 141 AlaIleThrGluSerAspPhePheIleAsnGlySerAsnThrGluGlyIleLeuGly 160
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Db 789 GCCATCTGATATAGACAAAGTTCTTCATCAACGGCTCCAACTGGAAAGGATCTTGGGG 848
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180
|||
Db 849 CTGGCTATGTGTGATGTGCAGGCTGACGACATCCCTGGAGGCTTTCTTGAATCTCTG 908
QY 181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCysGlyAlaGlyPhePro 200
|||
Db 909 GTAAAGAGAACCCACGTTCCCACTTCTCCCTGCAAGCTTGTGTGCTGGGCTTCCCC 968
QY 201 LeuAsnGlnSerGluValIleuAlaSerValGlyGlySerMetIleIleGlyIleAsp 220
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Db 969 CTCAACCAAGTCTGAAGTCTGGCTCTGTGCGAGGGAGCATGATCATTTGAGATGTGAC 1028
QY 221 HisSerLeuTyrThrGlySerLeuTyrThrProIleArgArgIleTyrTyrGlu 240
|||
Db 1029 CACTCGCTGATACAGGCAAGCTCTGGTATATACCCATCCGGCGGAGTGTATTATGAG 1088
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysGlyGluTyr 260
|||
Db 1089 GTGTATCATTTGGCCGGTGGAGATCAATGACAGGATCTGAAATGACCTCCAAAGAGTAC 1148
QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysLeuVal 280
|||
Db 1149 AACTATGACAAAGACATTGAGAGTGGACCAACCACTTCTGTTGGCCCAAGAAAGTG 1208
QY 281 PheGluAlaValIleValSerIleLeuAlaAspSerThrGluLysPheProAspGly 300
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Db 1209 TTTAAGCTGCAAGCAATCATCATCAAGGCAAGCCCTCCACGAGAAAGTTCCGTATGCT 1268
QY 301 PheTyrLeuGlyGluGlnLeuValCysTyrGlnAlaGlyThrThrProTyrAsnIlePhe 320
|||
Db 1269 TTCTGGCTAGAGAGCAGCTGTGTGTCTGGCAGCAGGCAACCCCTTGAACATTTTC 1328
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
|||
Db 1329 CCAATCATCTCACTCATCTATGTGGTGAAGTTTACCAACGATCTTCCGATATCAATC 1388
QY 341 LeuProGlnGlnTyrLeuArgProValGluLysValAlaThrSerGlnAspAspCysTyr 360
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QY	281	PheGluAlaAlaValIysSerIleValAlaIasSerThrGluIysPheProAspIy	300
Db	2004	TTGAGAGTGCAGTCMAATTCATCAGGACGCTCTCCAGGAGAAATTCCTGATGT	1945
QY	301	PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyIYrThrProTrpAsnIlePhe	320
Db	1944	TTCTGGCTAGAGAGACCACTGGTGTGGTCGACAGCAGCACCACTCCCTGGAAACTTTTC	1885
QY	321	ProValIIeserLeuYrLeuMetGlyValuValThrAsnIYserPheArgIleThrIle	340
Db	1884	CCAGCATCTCACTTACCTATATGGGTATGGTTACCAACAGTCTTCGCAATCACATC	1823
QY	341	LeuProGlnGlnYrLeuArgProValGluAspValAlaThrSerGlnAspAspCysYr	360
Db	1824	CTTCGGCAGCAATACCTCGGGCAGATGGAATGTGGCCACGTCACAGACGACTGTAC	1765
QY	361	LysPheAlaIleSerGlnSerSerThrGlyIYrValMetGlyAlaValIleMetGluGly	380
Db	1764	AAGTTGGCACTCTCACTCATCCACGGGCACTGTTAAGGGAGCGCTGATATATGAGGGC	1705
QY	381	PheYrValIValPheAspArgAlaArgIYsArgIleGlyPheAlaValSerIleCysHis	400
Db	1704	TTCTACGTGCTCTTGATCGGGCCCGAATAAGATGGCTTGTGCTGATAGCGCTTGCCAT	1645
QY	401	ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu	420
Db	1644	GTCGACGATGAGTTTCAGACGCGACGGGTGGAAAGCCCTTTTGTTCACCTTGACATGGA	1585
QY	421	AspCysGlyYrAsnIleProGlnThrAspGlnSerThr	433
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2005, 00:24:09 ; Search time 8190 Seconds
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	2267	99.1	1527	6 BD103723	BD103723 Beta Secr

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6	2267	99.1	2070	6 AR269224	AR269224 Sequence
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8	2267	99.1	2070	6 AR487345	AR487345 Sequence
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11	2267	99.1	2070	6 AR560095	AR560095 Sequence
12	2267	99.1	2070	6 AX700447	AX700447 Sequence
13	2267	99.1	2070	6 AR200343	AR200343 Homo sapi
14	2267	99.1	2348	6 AR404203	AR404203 Sequence
15	2267	99.1	2348	6 AR404204	AR404204 Sequence
16	2267	99.1	2526	6 AX700446	AX700446 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6627739.
ACCESSION AR404163
VERSION AR404163.1 GI:40152203
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1503)
AUTHORS Anderson,U.P., Basl,G., Doan,M.T., Frigon,N., John,V., Power,M.,
Sinha,S., Tatsuno,G., Tung,J.J., Wang,S. and McConlogue,L.
TITLE .beta.-secretase enzyme compositions and methods
JOURNAL Patent: US 6627739-A 1 30-SEP-2003;
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source location/Qualifiers
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ORIGIN

Alignment Scores:
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Best Local Similarity: 99.08% Mismatches: 1
Query Match: 99.08% Indels: 0
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US-10-726-967a-84 (1-433) x AK404163 (1-1506)

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 Db CGGCTGCCCCGGGAGACCGACGAGAGCCCGAGAGCCCGGCGGAGGGGAGCTTTGTG 183
 QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
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 QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
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 QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
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 QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLeuAspGly 260
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 QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
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 QY 281 PheGluAlaAlaValLysSerIleLeuValAspSerThrGluLysPheProAspGly 300
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 QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360

Db 1084 CTTCGACAGCAATACCTGGCGCCAGTGGAAAGATGTGCCACAGTCCCAAGACGATGTAC 1143
 QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
 Db 1144 AGTTTGCCATCTTCAAGATCAATCCAGGCGACCTGTATAGGAGCTGTATATATAGAGGGC 1203
 QY 381 PheTyrValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
 Db 1204 TTCTAGCTTGTCTTGTATCGGGCCGAAAGAAATGGCTTTGCTGTCAAGGCTTGCCAT 1263
 QY 401 ValHisAspGluPheAspThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
 Db 1264 GTGACAGATGATTCAGAGCGAGCGGTGGAGAGCCCTTTTGTCACTTGACATGAA 1323
 QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
 Db 1324 GACTGTGCTTCAACATTTCCACAGACAGATGATCAACC 1362

RESULT 2
 AX700448 1506 bp DNA linear PAT 03-APR-2003
 LOCUS
 Sequence 3 from Patent WO03012089.
 DEFINITION
 AX700448
 ACCESSION
 AX700448.1 GI:29536239
 VERSION
 AX700448.1 GI:29536239
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1
 Yon, J., Cleasby, A., Bruinzeel, W.D., Measure, S.L., Tickle, I. and
 Shariff, A.
 Crystal structure of beta-site app cleaving enzyme (bace) and use
 thereof
 Patent: WO 03012089-A 3 13-FEB-2003;
 Aetex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)
 FEATURES
 location/Qualifiers
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 /organism="Homo sapiens"
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 source

ORIGIN
 Alignment Scores:
 Pred. No.: 1e-197 Length: 1506
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 6 Gaps: 0

US-10-726-967a-84 (1-433) x AX700448 (1-1506)

QY 1 ThrGlnHISGlyTlleArgLeuProLeuArgSerGlyLeuGlyGlyAlaProLeuGlyLeu 20
 Db ACCACGACGCGGATCCGGCTCGCTGGCGACGGCCCTGGGGGGCGCCCTGGGGCTG 123
 QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyAlaArgGlySerPheVal 40
 Db CGGCTGCCCCGGGAGACCGACGAGAGCCCGAGAGCCCGGCGGAGGGGAGCTTTGTG 183
 QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
 Db GAGATGGTGACAACTGAGGGGCAAGTCGGGGGCAAGGCTTCTGCTGAGATGACCGTG 243
 QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
 Db GGCAGCCCCCGGACGAGCTCAACATCTGGTGATACAGGACAGCACTTTCAGTG 303
 QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
 Db GGTCTGCCCCCGACCCCTTCCTGCTATGCTACTACAGAGGAGCGCTGTCACACATAC 363

DB 304 GGTGCTGCCCCCACCCTCTCTGATGCTACTACAGAGGACAGCTGTCCAGACATAC 363
QY ArgApPLeuAaRgLyGgLyValTyRValProTyRThRgInGlyLysTPGInGlyLLeu 120
DB 364 CGGAGACTCCGGAGAGGAGTGTGATGTGCTTACACCCAGGAGCAAGTGGAGAGGAGACTG 423
QY 121 GYThRAsPLeuValSerLleProHlAgLyProAbnValThRValAaRgAlaAenLleAla 140
DB 424 GGCACGACCTGTGTAAGCATCCCCATGCCCCAACGCTACTGTGCGCTGCACATGTCT 483
QY 141 AlaIeThRgIuSerAsPLeuPhePheLleAenGlySerAenTPGInGlyLleLeuGly 160
DB 484 GCCATCACTGAATCAGACAACTTTCTTACTACAGGCTCCAACTGGAGAGCATCTG969 543
QY 161 LeuAaTyRAlaGlyLleAlaAaRgProAbnAsPLeuGInuProPheAsPLeu 180
DB 544 CTGGCTTAATGTGAGATTCAGAGGCTGACGACTCCCTGGAGCTTTCTTGACTCTG 603
QY 181 ValTyGInThRHisValProAbnLeuPheSerLeuGInuCySGLyAlaGlyPhePro 200
DB 604 GTAAAGAGACCCACGTTCCCAACCTCTCTCCCTGAGCTTGTGTGCTGCTTCC 663
QY 201 LeuAenGInuSerGInuValLeuAaSerValGlyGlySerMetLleLleGlyGlyLeaP 220
DB 664 CTCAACCAAGTGTGAAGTGTGCTGCTGTGAGAGGAGCATGATCATTGGAGTATCGAC 723
QY 221 HisSerLeuTyRThRgIuSerLeuTyRThRProLleAaRgAluTyRtyRgIn 240
DB 724 CACTCGCTTACACAGGAGCATCTGTGTATACCCATCGGAGGAGTGTATATGAG 783
QY 241 ValLleLeValAaRgValGlyLleAenGlyLleAsPLeuLysMetAsPLeuGlyGly 260
DB 784 GTGATCATGTGTGGGGTGGAGATCATAGACAGATCTGAAAATGACCTGCAGAGATAC 843
QY 261 AsnTyRAsPLeuSerLleValAaPLeuSerGlyThRThRAsnLeuArgLeuProLysVal 280
DB 844 AACATAGACAAAGACATGTGTGACAGTGGCACCAACCTTGTTCACCAAGAAAGT 903
QY 281 PheGlyAlaAlaValLysSerLleLysAlaAlaSerSerThRgInuPheProAsPly 300
DB 904 TTGGAAGCTGCAGTCAAAATCCATCAAGGAGCCTCTCCACGAGAGATTCCTGATGAT 963
QY 301 PheTPLeuGlyGInuLeuValCyTPGInAlaGlyThRThRProTPAsnLlePhe 320
DB 964 TTCTGCTAGAGAGACGCTGGTGTCTGCAAGGAGGACACCTTGGAAACATTTTC 1023
QY 321 ProValLleSerLeuTyRLeuMetGlyGlyValThRAsnGInuSerPheArgLleThRle 340
DB 1024 CCAATCATCTCACTTAACTTAATGGTGAAGTTTACCAACCAATCTTCCTCCATCACCATC 1083
QY 341 LeuProGInuGInuTyRLeuArgProValGlyAaPLeuValAlaThRSerGlyAsPLeuCy 360
DB 1084 CTTCGCGACAAATACCTGCGGCGAGTGGAGATGTGGCACCTCCCAAGACACTGTATC 1143
QY 361 LysPheAlaAlleSerGInuSerSerThRgLyThRValMetGlyAlaValLleMetGly 380
DB 1144 AAGTTTGCATCTCAAGTCAATCCAGGCGACCTGTTATAGGAGCTGTTATCATGAGAGGC 1203
QY 381 PheTyRValAlaPheAsPLeuAlaRgLyAaRgLyLleGlyPheAlaAlaSerAlaCyHis 400
DB 1204 TTCTAGCTTGTCTTGTGATCGGGCCGAAAGCAATGTGCTTGTGCTAGGCTTGCAT 1263
QY 401 ValHisAsPLeuPheAaRgThRAlaAlaValGlyGlyProPheValThRLeuAsPLeuGly 420
DB 1264 GTGACAGATGAGTTCAGAGCGGACGGTGGAGAGCCCTTTGTACACTTGGACATGGAA 1323
QY 421 AsPLeuGlyTyRAsnLleProGInuThRAsPLeuSerThR 433
DB 1324 GACTGTGCTTACAACTTCCACAGACAGATGATGATCAAC 1362
RESULT 4
BD103723.

LOCUS BD103723 1527 bp DNA linear PAT 27-AUG-2002
DEFINITION Beta secretase inhibitor.
ACCESSION BD103723
VERSION BD103723.1 GI:22649297
KEYWORDS WO 0187293-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Miyamoto, M., Maceui, J., Fukumoto, H. and Tarru, N.
TITLE Beta secretase inhibitor
JOURNAL Patent: WO 0187293-A 6 22-NOV-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, MASAO MIYAMOTO, JUNJI MATSUI,
HIROAKI FUKUMOTO, NAOKI TARUI
COMMENT OS Homo sapiens (human)
PN WO 0187293-A/6
PD 22-NOV-2001
PF 18-MAY-2001 WO 2001JP004144
PR 19-MAY-2000 JP 00P 152758
PI MASAO MIYAMOTO, JUNJI MATSUI, HIROAKI FUKUMOTO, NAOKI TARUI
PC 4164' A61K31/00, A61P25/00, A61P25/16, A61P25/28
CC Beta secretase inhibitor
FH Key location/Qualifiers
FT source 1..1527
FT location/Qualifiers
FT source 1..1527
FT /organism='Homo sapiens (human)'.
ORIGIN
Alignment Scores:
Pred. No.: 1,02e-197 Length: 1527
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0
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QY 1 ThRGlHisGlyLleArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
DB 64 ACCACACAGGACATCCGCTGCCCTGGCGACAGGCTGGGGGGGCCCCCTGGGGCTG 123
QY 21 GInuLleAsnLeuGInuThRAsPLeuGInuProGInuGlyLysArgGlySerPheVal 40
DB 124 CGGCTGCCCCGGAGAGCCGACAGAGAGCCCGGAGGAGCCCGGAGGAGGAGCTTTGTG 183
QY 41 GluMetValAsPAsnLeuArgGlyLysSerGlyGInuTyRtyRValGluMetThRVal 60
DB 184 GAGATGTGGAACAATGAGGGGCAAGTCGGGCGAGGCTACTAGTGAATGACCTG 243
QY 61 GlySerProProGInuThRLeuAsnLleLeuValAsPThRgIySerSerAsnPheAlaVal 80
DB 244 GGCAGCCCCCGACACGCTCAACATCTGTTGATACAGGACAGCACTTGTGACGTG 303
QY 81 GYAlaAlaProHisProPheLeuHisArgTyRtyRgInuArgInuSerSerThRtyR 100
DB 304 GGTGCTGCCCCCACCCTCTCTGATGCTACTACAGAGGAGCTGTCCAGACATAC 363
QY 101 ArgApPLeuAaRgLyGgLyValTyRValProTyRThRgInGlyLysTPGInGlyLLeu 120
DB 364 CGGAGACTCCGGAGAGGAGTGTGATGTGCTTACACCCAGGAGCAAGTGGAGAGGAGACTG 423
QY 121 GYThRAsPLeuValSerLleProHlAgLyProAbnValThRValAaRgAlaAenLleAla 140
DB 424 GGCACGACCTGTGTAAGCATCCCCATGCCCCAACGCTACTGTGCGCTGCACATGTCT 483

QY 141 AlaIleThrGluSerAspIysPhePheIleAengIysSerAsnTrpGluGlyIleLeuGly 160
Db 484 GCCATCACTGATCAAGACAAAGTTCTTCAACACGGCTCCACATGGGAAGGCACTGGGG 543
QY 161 LeuAlaTrpAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCCATTGCTGAATTGGCCAGGCTTACAGACTCCCTGGAGCTTTCTTGACTCTCG 603
QY 181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCysGlyValaGlyPhePro 200
Db 604 GTPAAGCAGACCAAGTCCCAACCTCTTCTCCCTGACAGCTTGGTGGCTGGCTCCCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValaGlyGlySerMetIleIleGlyIleLeuP 220
Db 664 CTCACACCAAGTCAAGTGTGGCTCTGTGCGAGGAGAGATGATCATGAGAGATACGAC 723
QY 221 HisSerLeuTrpThrGlySerLeuTrpTrpThrProIleArgAluTrpTrpTrpGlu 240
Db 724 CACTGCTGTACACAGGACAGTCTCTGGTATACACCATCCGCGGGAGTGGTATTTAG 783
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QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
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QY 321 ProValIleSerLeuTrpLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
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Db 1084 CTTCCGACCAAACTGTGGCGGCAAGTGAAGATGGCCAGTCCCAAGACATCTTAC 1143
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Db 1204 TTCTACGTTGTCTTATCGGGCCGAAAAAGAAATTGGCTTGTGTGACGCTTCCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValaGluGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGCACGATGAGTTCAGAGACGCGAGGGTGAAGGCCCTTTTGTCACTTGGACATGAA 1323
QY 421 AspCysGlyTrpAsnIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTAAACATTTCCACAGACAGATGATCAACC 1362
RESULT 5
AR224093 2070 bp DNA linear PAT 26-SEP-2002
LOCUS AR224093 Sequence 3 from patent US 6440698.
DEFINITION AR224093
ACCESSION AR224093
VERSION AR224093.1 GI:23332753
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M.E., Bienkowski,M.J., Heintz,Koon,R.L., Parodi,L.A. and Yan,R.

TITLE Alzheimer's disease secretase, APP substrates therefor, and uses therefor
JOURNAL Patent: US 6440698-A 3 27-AUG-2002;
FEATURES Location/Qualifiers
SOURCE 1..2070
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.5e-197 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: Gaps: 0
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QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
Db 124 CGGCTGCCCGGGAGACCGAGAGAGCCCGAGAGCCCGGCGGAGGGGAGCTTGTG 183
QY 41 GluMetValaAspAsnLeuArgGlyLysSerGlyGlnGlyTrpTrpValaGluMetThrVal 60
Db 184 GAGATGGTGAACAACCTAGAGGGGCAAGTCCGGGGGCGGCTACTAGTGAATGACCGTG 243
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QY 141 AlaIleThrGluSerAspLysPhePheIleAengIysSerAsnTrpGluGlyIleLeuGly 160
Db 484 GCCATCACTGATCAAGACAAAGTTCTTCAACACGGCTCCACATGGGAAGGCACTGGGG 543
QY 161 LeuAlaTrpAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
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QY 181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCysGlyValaGlyPhePro 200
Db 604 GTPAAGCAGACCAAGTCCCAACCTCTTCTCCCTGACAGCTTGGTGGCTGGCTCCCC 663
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QY 221 HisSerLeuTrpThrGlySerLeuTrpTrpThrProIleArgAluTrpTrpTrpGlu 240
Db 724 CACTGCTGTACACAGGACAGTCTCTGGTATACACCATCCGCGGGAGTGGTATTTAG 783
QY 241 ValIleIleValaArgValaGluIleAengIyGlnAspLeuLysMetAspCysAlysGluTr 260
Db 784 GTGATCATTTGTGGGGTGGAGATCATAGACAGGATCTGAATGAGACTGCAGAGAGTAC 843
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Db 904 TTGTGAAGCTGACGTAACATTCATCAAGGACGCTCTCCACGAGAAAGTTCCGATGGT 963
Qy 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnIleGlyThrThrProTrpAsnIlePhe 320
Db 964 TTCTGGCTGAGAGACGACGCTGTGTGTGCTGCACAGACACACCCCTTGGAACATTTTC 1023
Qy 321 ProValIleSerIleThrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAGCATCTCATCTACTACTAATGAGGTTCACCAACAGTCTTCCCATCACCATC 1083
Qy 341 LeuProGlnGlnIleThrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTrp 360
Db 1084 CTTCCGACGAAATACCTGCGCGCCAGTGAAGATGTGCCACGTCCTCCAAAGACGCTGTAC 1143
Qy 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1144 AAGTTTGCATCTCATAGCTCATCCAGGCACTGTTATGGAAGCTGTTATCATGAGGGC 1203
Qy 381 PheTrpValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1204 TTCTACGTTGCTTTGATCGGCGCCGAAACGAATTGGCTTGTCTGTCAAGCCGTTCCAT 1263
Qy 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGCACATATGATTCAGAGACGCGACGCGTGAAGGCCCTTTGTCTACCTTGACATGAGA 1323
Qy 421 AspCysGlyIleThrAsnIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTACAAACATTCACAGACGATGACTCAAC 1362

RESULT 6
LOCUS AR269224 2070 bp DNA linear PART 10-APR-2003
DEFINITION Sequence 3 from patent US 650667.
ACCESSION AR269224
VERSION AR269224.1 GI:29700192
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M.E., Bienkowiak,M.J., Heinrikson,R.L., Parodi,L.A. and Yan,R.
TITLE Aspartyl protease 2 (Asp2) antisense oligonucleotides
JOURNAL Patent: US 650667-A 3 31-DEC-2002;
FEATURES
source location/Qualifiers
1..2070
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1,5e-197 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservatave: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 6 Gaps: 0
US-10-726-967a-84 (1-433) x AR269224 (1-2070)

Qy 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
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Qy 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyArgArgIleSerPheVal 40
Db 124 CGGCTGCCCGGAGACCGACGAAAGAGCCCGAGAGAGCCGCGCGGAGGGCAGCTTGTG 183

Qy 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyIleThrValGluMetThrVal 60
Db 184 GAGATGTGTGACAACTGAGGGGCAAGTCGGGCGAGGCTACTACGTGAATACACCTGT 243
Qy 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 244 GGCAGCCCCCGCAGACCTCAACATCTCGTGTGATACAGCAGACAGTAACCTTGGCATG 303
Qy 81 GlyAlaAlaProHisAspPheLeuHisArgTrpIleGlnArgGlnLeuSerSerThrTrp 100
Db 304 GGTGTGCCCCCACCACCTTCTGTGATGCTTACACAGAGGCGCTGTCCAGCACATAC 363
Qy 101 ArgAspLeuArgLysGlyValTrpValProTrpThrGlnGlyLysTrpGluGlyLeu 120
Db 364 CGGAGCTCCGGAAGGGGTGTATGTGCTTACACCCAGGCAAGTGGAAAGGGAGCTG 423
Qy 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 424 GGCACCGACCTGTGAAGCATCCCATGAGCCCAACCTCATCTGTGCGCAACATGTCT 483
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Qy 161 LeuAlaTrpAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCTATGTGTGATGTGCGAGGCTGACGACATCTCCCTGAGCTTCTTGTGACTCTG 603
Qy 181 ValLysGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValGlyPhePro 200
Db 604 GTAAAGCAGACCCACGTTCCCAACCTTCTCTCTGAGCTTGTGTGTGCTTGTCTTCCC 663
Qy 201 LeuAsnGlnSerGluValLeuAlaSerValGlyLysMetIleIleGlyGlyIleAsp 220
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Qy 221 HisSerLeuTrpThrGlySerLeuTrpTrpThrProIleArgArgIleTrpTrpGlu 240
Db 724 CACTCGCTGACAGGACGACGCTCTGTGTATACACCATCCGCGGAGGTGATATATGAG 783
Qy 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLysGluTrp 260
Db 784 GTCATCATTTGTGGGTGGAGATCATGACAGATCTBAATAATGACTGCAAGAGATAC 843
Qy 261 AsnTrpAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 844 AACTATGACAAAGCATTTGTGACGATGGCACACCAACCTTCGTTGCCAAAGAAAGTG 903
Qy 281 PheGluAlaAlaValIleSerIleLeuValAlaIleSerThrGluLysPheProAspGly 300
Db 904 TTGTGAAGCTGACGTAATCCATTCAGGACGCTCTCCACGGAAGTTCCTGATGAGT 963
Qy 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnIleGlyThrThrProTrpAsnIlePhe 320
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Db 1084 CTTCCGACGAAATACCTGCGCGCCAGTGAAGATGTGCCACGTCCTCCAAAGACGCTGTAC 1143
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Qy 381 PheTrpValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1204 TTCTACGTTGCTTTGATCGGCGCCGAAACGAATTGGCTTGTCTGTCAAGGCTTGCAT 1263
Qy 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420

Db 1264 GTGCAGATGAGTTCAGGACGGCAGCGGGAAGGCGCTTTGTGCACTTGGACATGGAA 1323
Qy 421 AAPPYSGLYTYRASN1LEPROGINTHRASPGLUSERTHR 433
Db 1324 GACTGTGCTACACATTCACAGACAGATGAGTCAACC 1362

RESULT 7
AR478778
LOCUS AR478778 2070 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 3 from patent US 6699671.
ACCESSION AR478778
VERSION AR478778.1 GI:47237498
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrichson,R.L., Parodi,L.A. and
Van,R.
TITLE Alzheimer's disease secretase, APP substrates therefor, and uses
therefor
JOURNAL Patent: US 6699671-A 3 02-MAR-2004;
FEATURES Location/Qualifiers
source 1..2070
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.5e-197 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: Gaps: 0

US-10-726-967a-84 (1-433) x AR478778 (1-2070)

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Db 64 ACCACACAGGACATCCGGCTGCGCCGCGACGGCTGGGGGGCCCCCTGGGGCTG 123
Qy 21 GIULIEASNLEUGLINTHRAPGLUGLUPROGLUGLUPROGLIYARGHARGGLYSERPHEVA 40
Db 124 CGGCTCCCGCGAGACCGACGAGAGCCGCGAGACCCGCGAGGGCAGCTTTGTC 183
Qy 41 GLUMETVALASPANLEUARGLYLYSERGLYGLNGLYTYRTYRVALGIUMETTHRVA 60
Db 184 GAGATGCTGACAACTGAGGGGCAAGTCGGGGCAGGGCTACCTGAGATGACCTG 243
Qy 61 GLYSEPRORGLINTHRAENIILEUVALASPTHRGLYSERSEANPHEALVA 80
Db 244 GGGAGCCCCCGAGAGCGCTCAACATCTGGTGATACAGGCAAGCTTTCAGTC 303
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Db 304 GGGCTGCCCCCAACCCCTTCCTGCAATCGCTACCAAGAGGAGCTGTCCAGCATAC 363
Qy 101 ARGASPLEUARGLYGLYVALIYRVALPROTYRTHGLNGLYLYSTPGLUGLYGLUEN 120
Db 364 CGGAGCTCCGGAAGGCTGTGTGTGCTTACACCCAGGGAAGTGGGAAGGGAGCTG 423
Qy 121 GLIYTHRAPLEUVALSERILEPROHISGLYPROASNVALTHRALAANILEALA 140
Db 424 GGGACGCACTGGTGAAGCATCCCAAGGCCCAAGCTCACTGTGCTGCCAATTCCT 483
Qy 141 ALAILETHRGLUSERAPLYSPHEPHEILEASNGLYSERASNTIPGLUGLYILEUGLY 160
Db 484 GCCATCACTGAATCAGACAAAGTTCTTCATCAAGGGCTCCAACTGGGAAGCATCTGG 543
Qy 161 LEUVALTYRALGLIUILEALARGPROASPASPERSERLEUGLUPROPHLEAPSERLEU 180

Db 544 CTGGCTATGCTGAGATTCAGGACCTGACGATCCCTTGAGCCCTTTTGACTCTCTG 603
Qy 181 VALLYSGINTHRHISVALIPROASNLEUPHSEULEUGLILEUCYSGLYVALAGLYPHEPRO 200
Db 604 GTAAAGGAGACCAAGTTCACACCTCTTCCCTGGACGCTTGGGCTTGGCTTCCCC 663
Qy 201 LEUANGINSEKGLIUALLEUALASERVALGLYGLYSERMETILEGLYGLI1EASP 220
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Db 724 CACTGCTGTACAGAGGAGCTCTGTGATACCCATCCGCGGAGAGTGTATATAG 783
Qy 241 VALILEILEVALARGVALGLIUILEASNGLYGLINAPLEUYSMEASPGLYSGLUTYR 260
Db 784 GTCAATCATTCGCGGTGTGAATCAATGACAGGATTCGAAAATGACTGCAAGAGATAC 843
Qy 261 ASNTYRASPGLYSERILEVALASPSEKGLYTHRTHRAENLEUARGLEUPROLYSEVAL 280
Db 844 AACTATGACAGAGCATTTGTGACAGTGGCACACCAACCTTCCTTCCCAAGAACTG 903
Qy 281 PHEGLUALAIALVALYSEKILEYSAIALASERSEKTHGLULYSPHEPROASPGLY 300
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Qy 321 PROVALI1ESERLEUTYRLEUMEGLYGLIUALTHRAANGINSEKPHARGILETHRILE 340
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Qy 341 LEUPROGLINGLYRLEUARGPROVALI1ULASPVALI1ATHRSEKGLIASPAPCYSTYR 360
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Qy 401 VALHISAPGLUPHEARGTHRZIALAVALI1GLUGLYPROPHEVALI1THLEUASPHEGLU 420
Db 1264 GTGCAGATGAGTTCAGAGCGGCAAGGGTGGAAAGCCCTTTGTCACTTGGACATGGAA 1323
Qy 421 AAPPYSGLYTYRASN1LEPROGINTHRASPGLUSERTHR 433
Db 1324 GACTGTGCTACACATTCACAGACAGATGAGTCAACC 1362

RESULT 8
AR487345
LOCUS AR487345 2070 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 3 from patent US 6706485.
ACCESSION AR487345
VERSION AR487345.1 GI:47252443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrichson,R.L., Parodi,L.A. and
Van,R.
TITLE Method of identifying agents that inhibit APP processing activity
JOURNAL Patent: US 6706485-A 3 16-MAR-2004;
FEATURES Location/Qualifiers
source 1..2070
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1,5e-197 Length: 2070
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 6 Gaps: 0

US-10-726-967a-84 (1-433) x AR487345 (1-2070)

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Db CGCGTGGCCCGGAGAGACGACGAAAGAGCCGAGGAGCCGCGCGGAGGGGCACTTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyIleValGlyMetThrVal 60
Db GAGATGTGACAACTGAGAGGCGAAGTCCGAGGAGGCTTACCTGAGATGACCGTG 243
QY 61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db GGCAGCCCCCGGAGAGCGTCAACATCTGTGGATACAGGACGACTTTCGAGTG 303
QY 81 GlyAlaIleAlaProHisProPheLeuHisArgIleValGlnArgGlnLeuSerSerThrIle 100
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Db CGGGAGCTCCGGAAGGTGTGTATGTCCCTTACACCGAGGAGAGTGGAGAGGAGCTG 423
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QY 141 AlaIleThrGlnSerAspLysPhePheIleAsnGlySerAsnThrGlnGlyIleLeuGly 160
Db GCCATCTACGATCAACAAAGTCTTCATCAACGAGCTTCAACCTGGAGAGGACCTCGGG 543
QY 161 LeuAlaIleValAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db CTGGCTTATGTGATGATGATGCGAGGCTGACGACTCCCTGAGACCTTTCTTTATCTCTG 603
QY 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro 200
Db GTPAAGCAACCCCACTTCCCACTTCTTCCCTGCACTTGTGTGCTGGCTTCCCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyIleAsp 220
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QY 221 HisSerLeuThrGlySerLeuThrIleProIleArgArgGluThrIleGlyGlu 240
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QY 241 ValIleIleValArgValGluIleAsnGlyIleAspLeuLysMetAspCysLeuGlyIle 260
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QY 261 AsnIleAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysLeuVal 280
Db AACCTATGACAAAGACATGTGACAGTGGACACCACTTCTGTTTCCCAAGAAAGTG 903
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QY 341 LeuProGlnGlyThrLeuArgProValGluAspValAlaThrSerGlnAspAspCysThr 360
Db 1084 CTTCCGACGACATATCTCGGCGAGTGGAAATGTGGCGACAGTCCCAAGACAGCTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGlyIle 380
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QY 381 PheIleValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
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QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
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RESULT 9

AR531984

LOCUS

Sequence 3 from patent US 6727074.

DEFINITION

AR531984

ACCESSION

AR531984.1

VERSION

GI:53920518

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 2070)

AUTHORS

Gurney,M.E., Bienkowski,M.J.,

Heinrikson,R.L., Parodi,L.A. and

Yan,R.

Alzheimer's disease secretase, APP substrates therefor, and uses

therefor

Patent: US 6727074-A 3 27-APR-2004;

JOURNAL

Patent: US 6727074-A 3 27-APR-2004;

FEATURES

Location/Qualifiers

1..2070

source

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 1,5e-197 Length: 2070
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 6 Gaps: 0

US-10-726-967a-84 (1-433) x AR531984 (1-2070)

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 QY 121 GLYTHASPLEUVALSERILEPROHISGLYPROASNVALTHRYVALARGLAASNILEALA 140
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 LOCUS AR540886 2070 bp DNA linear PAT 08-OCT-2004
 DEFINITION Sequence 3 from patent US 6737510.
 ACCESSION AR540886
 VERSION AR540886.1 GI:53932399
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 2070)
 Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
 Yan,R.
 Alzheimer's disease secretase, APP substrates thereof, and uses
 thereof
 Patent: US 6737510-A 3 18-MAY-2004;
 Location/Qualifiers
 1..2070
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1,5e-197 Length: 2070
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: Gaps: 0
 US-10-726-967a-84 (1-433) x AR540886 (1-2070)
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 QY 41 GIUMETVALASPSNUARGGLYLYSERGLYGLNGLYTYRTHRYVALGIUMETTHRYVAL 60
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QY 201 LeuAnGIInserGIuValLeuAlaSerValGIySerMetIleIleGIyIleAsp 220
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QY 241 ValIleIleValArgValGIuIleAnGIyGIuAspLeuIlyMetAspCysIlyGIuTYr 260
Db 784 GTCAATCATGTGGCGGTGAGATCAATGACAGGATCTGAATGACCTGCAAGAGAGTAC 843
QY 261 AsnTYrAspIlySerIleValAspSerGIyThrThrAsnLeuArgLeuProIlyIleVal 280
Db 844 AACTATGACAAAGGCAATGTGGACAGTGGCAACCACTTGTGGTGGCAAGAAAGT 903
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QY 401 ValHisAspGIuPheArgThrAlaAlaValGIuGIyProPheValThrIleuAspMetGIu 420
Db 1264 GTTCAGATGATGTTCTCAGAGCGGAGCGGTGAAGGCTTTTGTGCACCTTGACATGGAA 1323
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RESULT 11
ARS60095 2070 bp DNA linear PAT 08-OCT-2004
LOCUS ARS60095
DEFINITION Sequence 3 from patent US 6753163.
ACCESSION ARS60095
VERSION ARS60095.1 GI:53970462
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2070)
AUTHORS Gurney,M.E., Bienkowski,M.J., Heinrikson,R.L., Parodi,L.A. and
TITLE Alzheimer's disease secretase, APP substrates therefor, and uses
therefor
JOURNAL Patent: US 6753163-A 3 22-JUN-2004;
FEATURES
source location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Alignment Scores: 1..5e-197 Length: 2070
Pred. No.: 2267.00 Matches: 429
Score: *

Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 6 Gaps: 0
US-10-726-967a-84 (1-433) x ARS60095 (1-2070)
QY 1 ThrGIInHISGIyIleArgLeuProLeuArgSerGIyLeuGIyGIyAlaProLeuGIyLeu 20
Db 64 ACCGACGACGGCATCCGGCTGCCCTGTGGCGAGCGGCTCGGGGGGCGCCCTGGGGCTG 123
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Db 184 GAGATGTGTGACAACTGTAGGGGCAAGTCCGGGCGAGGCTTACGTGAGATGACCTG 243
QY 61 GIySerProProGIInThrIleuAsnIleuValAspThrGIySerSerAsnPheAlaVal 80
Db 244 GGCAGCCCCCGGACAGAGCTTCACATCTGTGTGATACAGGCAAGTAACTTGTGACGTG 303
QY 81 GIyAlaAlaProHISProPheLeuHISArgTYrTYrGIuArgGIuAspSerSerThrTYr 100
Db 304 GTGTGCTGCCCGCCACCCCTTCTGTGATCGTATCAACAGAGGAGCTGTCCAGACATAC 363
QY 101 ArgAspLeuArgIyGIyValTYrValProTYrThrGIuGIyTYrTYrGIuGIyGIuLeu 120
Db 364 CGGACCTCCGGAAGGGGTGTGTATGTGCTTACACCCAGGGCAAGTGGAAAGGGAGCTG 423
QY 121 GIYThrAspLeuValSerIleProHISGIyProAsnValThrValArgAlaAsnIleAla 140
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QY 141 AlaIleThrGIuSerAspLysPhePheIleAsnGIySerAsnTYrGIuGIyIleGIuGIy 160
Db 484 GCATCACTGATCAGCAAGATTCTTTCATCAAGGGCTCCAACTGGAGAGGCATCTGGGG 543
QY 161 LeuAlaTYrArgIuIleAlaArgProAspAspSerLeuGIuProPheAspSerLeu 180
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QY 181 ValIySGInThrHISValProAsnLeuPheSerLeuGIuLeuGIyGIyAlaGIyPhePro 200
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Db 724 CACTCGCTGTACACAGGCAAGTCTGTGTATACACCATCCGGGGGAGTGTATTATGAG 783
QY 241 ValIleIleValArgValGIuIleAnGIyGIuAspLeuIlyMetAspCysIlyGIuTYr 260
Db 784 GTCAATCATGTGGCGGTGAGATCAATGACAGGATCTGAATGACCTGCAAGAGAGTAC 843
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RESULT 12

AX700447 2070 bp DNA linear PAT 03-APR-2003
 LOCUS AX700447
 DEFINITION Sequence 2 from Patent WO03012089.
 AX700447
 VERSION AX700447.1 GI:29536238
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
 Yon, J., Cleasby, A., Bruinzeel, W.D., Masure, S.L., Tickle, I. and
 Shaef, A.

TITLE Crystal structure of beta-site app cleaving enzyme (bace) and use
 thereof

JOURNAL Patent: WO 03012089-A 2 13-FEB-2003;
 Abex Technology Limited (GB) ; JANSSEN PHARMACEUTICA N.V. (BE)

FEATURES Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.: 1.5e-197 Length: 2070
 Score: 2267.00 Matches: 429
 Percent Similarity: 99.31% Conservative: 1
 Best Local Similarity: 99.08% Mismatches: 3
 Query Match: 99.08% Indels: 0
 DB: 6 Gaps: 0

US-10-726-967a-84 (1-433) x AX700447 (1-2070)

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 QY 101 ArgAspLeuArgLysGlyValTyrValProTyrThrGlnGlyLysTrpGlnGlyGluLeu 120
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 QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValAspAlaAsnIleAla 140
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 Db 844 AACTATGACAGAGCATTTGTGACGTGGACGTGCACACCAACTCTTCTTCCCAAGAAAGTG 903
 QY 281 PheGluAlaAlaValLysSerIleLysAlaIleAspSerThrGluLysPheProAspGly 300
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 Db 1264 GTGCACAGATGATTCAGACGCGCAGCGGTGGAAAGGCCCTTTGTCACTTGACATGGAA 1323
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 Db 1324 GACTGTGGCTACAACTTCACAGACAGATGAGTCAACC 1362

RESULT 13

AF200343
LOCUS AF200343 2070 bp mRNA linear PRI 12-DEC-1999
DEFINITION Homo sapiens chromosome 11 aspartyl protease 2 mRNA, complete cds.
ACCESSION AF200343
VERSION AF200343.1 GI:6561813
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2070)
Yan, R., Bienkowiak, M. J., Shuck, M. E., Miao, H., Torry, M. C.,
Pauley, A. M., Braehler, J. R., Stracman, N. C., Mathews, W. R., Buhl, A. E.,
Carter, D. B., Tomasselli, A. G., Parodi, L. A., Henriksen, R. L. and
Gurney, M. E.
TITLE
Membrane-anchored aspartyl protease with Alzheimer's disease
beta-secretase activity
JOURNAL Nature 402 (6761), 533-537 (1999)
MEDLINE 20057170
PUBMED 10591213
REFERENCE
2 (bases 1 to 2070)
Bienkowski, M. J., Shuck, M. E., Slightom, J. L. and Dong, R. F.
AUTHORS Direct Submission
JOURNAL Submitted (29-OCT-1999) Genomics Research, Pharmaciat&Upjohn, 301
Henrietta, Kalamazoo, MI 49007, USA
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Alignment Scores:
Pred. No.: 1.5e-197 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatch: 3
Query Match: 99.08% Indels: 0
Gaps: 0
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QY 41 GtUmetValAspAsnLeuArgGlyLySerSerGlyGlnGlyTyTyTyValGtUmetThrVal 60
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QY 61 GlySerProProGlnThrLeuAsnIleUeuValAspThrglySerSerAsnPhaAlaVal 80
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LOCUS Sequence 42 from patent US 6627739.
DEFINITION AR404203
ACCESSION AR404203
VERSION AR404203.1 GI:40152243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2348)
AUTHORS Anderson, J.P., Basi, G., Doan, M.T., Frigon, N., John, V., Power, M.,
Sinha, S., Tatsuno, G., Tung, J., Wang, S. and McConlogue, L.
TITLE .beta.-secretase enzyme compositions and methods
JOURNAL Patent: US 6627739-A 42 30-SEP-2003;
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Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0

US-10-726-967a-84 (1-433) x AR404203 (1-2348)

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RESULT 15
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LOCUS Sequence 44 from patent US 6627739.
DEFINITION AR404204
ACCESSION AR404204
VERSION AR404204.1 GI:40152244
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2348)
AUTHORS Anderson, J.P., Basi, G., Doan, M.T., Frigon, N., John, V., Power, M.,
Sinha, S., Tatsuno, G., Tung, J., Wang, S. and McConlogue, L.
TITLE .beta.-secretase enzyme compositions and methods
JOURNAL Patent: US 6627739-A 44 30-SEP-2003;
FEATURES
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Alignment Scores:
Pred. No.: 1 77e-197 Length: 2348
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: August 22, 2005, 00:19:29 ; Search time 1527 Seconds
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Listing first 45 summaries

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21: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2268	100.0	433	17	US-10-726-967A-84
2	2266	99.9	433	17	US-10-726-967A-81
3	2273	99.3	433	17	US-10-726-967A-78
4	2267	99.1	435	15	US-10-400-273-2
5	2267	99.1	456	16	US-10-281-092-8
6	2267	99.1	480	20	US-11-089-918-66
7	2267	99.1	480	20	US-11-090-866-66
8	2267	99.1	480	20	US-11-069-377-66
9	2267	99.1	480	20	US-11-090-872-66
10	2267	99.1	488	9	US-09-796-264-2
11	2267	99.1	488	9	US-09-845-226-2

12	2267	99.1	488	9	US-09-795-903A-2	Sequence 2, Appl1
13	2267	99.1	488	14	US-10-032-818-2	Sequence 2, Appl1
14	2267	99.1	488	16	US-10-820-853-2	Sequence 2, Appl1
15	2267	99.1	488	16	US-10-773-754-2	Sequence 2, Appl1
16	2267	99.1	501	14	US-10-032-818-4	Sequence 4, Appl1
17	2267	99.1	501	14	US-10-214-932-104	Sequence 104, App
18	2267	99.1	501	15	US-10-372-473-1	Sequence 1, Appl1
19	2267	99.1	501	15	US-10-652-927-4	Sequence 4, Appl1
20	2267	99.1	501	15	US-10-652-830-4	Sequence 4, Appl1
21	2267	99.1	501	16	US-10-281-092-6	Sequence 6, Appl1
22	2267	99.1	501	16	US-10-466-258-2	Sequence 2, Appl1
23	2267	99.1	501	16	US-10-652-045-4	Sequence 4, Appl1
24	2267	99.1	501	16	US-10-343-389A-19	Sequence 285, App
25	2267	99.1	501	16	US-10-723-860-285	Sequence 1, Appl1
26	2267	99.1	501	16	US-10-837-021A-1	Sequence 1, Appl1
27	2267	99.1	501	17	US-10-940-867-4	Sequence 1, Appl1
28	2267	99.1	501	17	US-10-726-967A-1	Sequence 1, Appl1
29	2267	99.1	501	18	US-10-466-391A-2	Sequence 2, Appl1
30	2267	99.1	501	20	US-11-089-918-2	Sequence 2, Appl1
31	2267	99.1	501	20	US-11-090-866-2	Sequence 2, Appl1
32	2267	99.1	501	20	US-11-069-377-2	Sequence 2, Appl1
33	2267	99.1	501	20	US-11-090-872-2	Sequence 2, Appl1
34	2267	99.1	503	9	US-09-796-264-3	Sequence 3, Appl1
35	2267	99.1	503	9	US-09-845-226-3	Sequence 3, Appl1
36	2267	99.1	503	9	US-09-795-903A-3	Sequence 3, Appl1
37	2267	99.1	503	14	US-10-032-818-3	Sequence 3, Appl1
38	2267	99.1	503	16	US-10-820-953-3	Sequence 3, Appl1
39	2267	99.1	503	16	US-10-773-754-3	Sequence 3, Appl1
40	2267	99.1	509	16	US-10-275-339A-7	Sequence 7, Appl1
41	2262	98.9	453	9	US-09-794-927-30	Sequence 30, Appl1
42	2262	98.9	453	9	US-09-795-847-30	Sequence 30, Appl1
43	2262	98.9	453	9	US-09-794-743-30	Sequence 30, Appl1
44	2262	98.9	453	9	US-09-794-746-30	Sequence 30, Appl1
45	2262	98.9	453	9	US-09-794-925-30	Sequence 30, Appl1

ALIGNMENTS

RESULT 1
US-10-726-967A-84
Sequence 84, Application US/10726967A
Publication No. US20050074456A1
GENERAL INFORMATION:
APPLICANT: Ballinger, Marcus
TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
FILE REFERENCE: 2004345-0021
CURRENT APPLICATION NUMBER: US/10/726,967A
CURRENT FILING DATE: 2003-12-02
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin version 3.2
SEQ ID NO 84
LENGTH: 433
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Soluble human PROBACE1 containing an engineered E1NL site
US-10-726-967A-84

Query Match 100.0%; Score 2268; DB 17; Length 433;
Best Local Similarity 100.0%; Pred. No. 4.5e-211; Indels 0; Gaps 0;
Matches 433; Conservative 0; Mismatches 0;
QY 1 TQHGIRLPRLSGIGAPLGLBINLTDEPERGRGSEFVEMVDNLRGSGGGYVEMTV 60
DB 1 TQHGIRLPRLSGIGAPLGLBINLTDEPERGRGSEFVEMVDNLRGSGGGYVEMTV 60
QY 61 GSPPTNLINLVDTGSSNFAVGAAPHPFLHRYRQRLSSTRDLRKGVVYPYTGKWEGL 120
DB 61 GSPPTNLINLVDTGSSNFAVGAAPHPFLHRYRQRLSSTRDLRKGVVYPYTGKWEGL 120


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Qy 121 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
|
|
|
Db 121 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
Qy 181 VKQTHVPLNLSIQLCGAGFPINQSEVLASVGGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
|
|
|
Db 181 VKQTHVPLNLSIQLCGAGFPINQSEVLASVGGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
Qy 241 VIVRVEINGODLKMDCKEYNVDKSIYDSGTTNLRPKKVFEEAAVKSIIKAASSTKEFPDG 300
|
|
|
Db 241 VIVRVEINGODLKMDCKEYNVDKSIYDSGTTNLRPKKVFEEAAVKSIIKAASSTKEFPDG 300
Qy 301 FMLEBQVLCWQAGTTPMNIIFPVISLYLMGEVYNOSFRITILLPOQYLRPEVDVATSODDCY 360
|
|
|
Db 301 FMLEBQVLCWQAGTTPMNIIFPVISLYLMGEVYNOSFRITILLPOQYLRPEVDVATSODDCY 360
Qy 361 KFAISQSGTGTWGAIVMEGFYVFDRAKRKIGFAVSACHVDEFRTAAVEGPFVTLTME 420
|
|
|
Db 361 KFAISQSGTGTWGAIVMEGFYVFDRAKRKIGFAVSACHVDEFRTAAVEGPFVTLTME 420
Qy 421 DCGYNIPQTDST 433
|
|
|
Db 421 DCGYNIPQTDST 433
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RESULT 2
US-10-726-967A-81
; Sequence 81, Application US/10726967A
; Publication No. US20050074456A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
; FILE REFERENCE: 2004345-0021
; CURRENT APPLICATION NUMBER: US/10/726,967A
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Soluble human proBACE1
US-10-726-967A-81
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Query Match 99.9%; Score 2286; DB 17; Length 433;
Best Local Similarity 99.8%; Pred. No. 7e-211;
Matches 432; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TOHGIRLPLRSGLGAPLGLLEINLETDEBEPEGRGSGFVEMVDNLRGKSGGQYVEMTV 60
|
|
|
Db 1 TOHGIRLPLRSGLGAPLGLLEINLETDEBEPEGRGSGFVEMVDNLRGKSGGQYVEMTV 60
Qy 61 GSPPQTLNIIIVDTGSSNFAVGAAPHPFLHRYRQRLSTYRDLRKGVVPTYGKMEGEL 120
|
|
|
Db 61 GSPPQTLNIIIVDTGSSNFAVGAAPHPFLHRYRQRLSTYRDLRKGVVPTYGKMEGEL 120
Qy 121 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
|
|
|
Db 121 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
Qy 181 VKQTHVPLNLSIQLCGAGFPINQSEVLASVGGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
|
|
|
Db 181 VKQTHVPLNLSIQLCGAGFPINQSEVLASVGGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
Qy 241 VIVRVEINGODLKMDCKEYNVDKSIYDSGTTNLRPKKVFEEAAVKSIIKAASSTKEFPDG 300
|
|
|
Db 241 VIVRVEINGODLKMDCKEYNVDKSIYDSGTTNLRPKKVFEEAAVKSIIKAASSTKEFPDG 300
Qy 301 FMLEBQVLCWQAGTTPMNIIFPVISLYLMGEVYNOSFRITILLPOQYLRPEVDVATSODDCY 360
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|
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Db 301 FMLEBQVLCWQAGTTPMNIIFPVISLYLMGEVYNOSFRITILLPOQYLRPEVDVATSODDCY 360
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Qy 361 KFAISQSGTGTWGAIVMEGFYVFDRAKRKIGFAVSACHVDEFRTAAVEGPFVTLTME 420
|
|
|
Db 361 KFAISQSGTGTWGAIVMEGFYVFDRAKRKIGFAVSACHVDEFRTAAVEGPFVTLTME 420
Qy 421 DCGYNIPQTDST 433
|
|
|
Db 421 DCGYNIPQTDST 433
```

```
RESULT 3
US-10-726-967A-78
; Sequence 78, Application US/10726967A
; Publication No. US20050074456A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Marcus
; TITLE OF INVENTION: Constructs for Homogenously Processed Preparations of Beta Site
; FILE REFERENCE: 2004345-0021
; CURRENT APPLICATION NUMBER: US/10/726,967A
; CURRENT FILING DATE: 2003-12-02
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Soluble human proBACE1 containing an engineered RLPL site
US-10-726-967A-78
```

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Query Match 99.3%; Score 2273; DB 17; Length 433;
Best Local Similarity 99.3%; Pred. No. 1.2e-209;
Matches 430; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 TOHGIRLPLRSGLGAPLGLLEINLETDEBEPEGRGSGFVEMVDNLRGKSGGQYVEMTV 60
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Db 1 TOHGIRLPLRSGLGAPLGLLEINLETDEBEPEGRGSGFVEMVDNLRGKSGGQYVEMTV 60
Qy 61 GSPPQTLNIIIVDTGSSNFAVGAAPHPFLHRYRQRLSTYRDLRKGVVPTYGKMEGEL 120
|
|
|
Db 61 GSPPQTLNIIIVDTGSSNFAVGAAPHPFLHRYRQRLSTYRDLRKGVVPTYGKMEGEL 120
Qy 121 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
|
|
|
Db 121 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
Qy 181 VKQTHVPLNLSIQLCGAGFPINQSEVLASVGGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
|
|
|
Db 181 VKQTHVPLNLSIQLCGAGFPINQSEVLASVGGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
Qy 241 VIVRVEINGODLKMDCKEYNVDKSIYDSGTTNLRPKKVFEEAAVKSIIKAASSTKEFPDG 300
|
|
|
Db 241 VIVRVEINGODLKMDCKEYNVDKSIYDSGTTNLRPKKVFEEAAVKSIIKAASSTKEFPDG 300
Qy 301 FMLEBQVLCWQAGTTPMNIIFPVISLYLMGEVYNOSFRITILLPOQYLRPEVDVATSODDCY 360
|
|
|
Db 301 FMLEBQVLCWQAGTTPMNIIFPVISLYLMGEVYNOSFRITILLPOQYLRPEVDVATSODDCY 360
Qy 361 KFAISQSGTGTWGAIVMEGFYVFDRAKRKIGFAVSACHVDEFRTAAVEGPFVTLTME 420
|
|
|
Db 361 KFAISQSGTGTWGAIVMEGFYVFDRAKRKIGFAVSACHVDEFRTAAVEGPFVTLTME 420
Qy 421 DCGYNIPQTDST 433
|
|
|
Db 421 DCGYNIPQTDST 433
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RESULT 4
US-10-400-273-2
; Sequence 2, Application US/10400273
; Publication No. US20040014194A1
```



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/ GENERAL INFORMATION:
/ APPLICANT: Beyer, Brian
/ APPLICANT: Hammond, Gerald S
/ APPLICANT: Reichert, Paul
/ APPLICANT: Strickland, Corey
/ APPLICANT: Wang, Wenyan
/ APPLICANT: Weber, Patricia C
/ APPLICANT: Wong, Gwendolyn
/ APPLICANT: Zhang, Lili
/ TITLE OF INVENTION: BETA-SECRETASE CRYSTALS AND METHODS FOR PREPARING AND USING THE S
/ FILE REFERENCE: J801531-K-US
/ CURRENT APPLICATION NUMBER: US/10/400,273
/ CURRENT FILING DATE: 2003-03-26
/ PRIOR APPLICATION NUMBER: 60/367,937
/ PRIOR FILING DATE: 2002-03-27
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 435
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-400-273-2

Query Match      99.1%; Score 2267; DB 15; Length 435;
Best Local Similarity 99.1%; Pred. No. 4,7e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TOHGRLPLRSGLGAPLGLINLETDEBERPGRGRGSFVEMVDNLRGSGGGYVEMTV 60
DB 1 TOHGRLPLRSGLGAPLGLRLPRETDEBERPGRGRGSFVEMVDNLRGSGGGYVEMTV 60
QY 61 GSPPTNLILVDTGSSNFAVGAAHPHPLHRYRQRLSTYRDLRKGVVPTYQKWEGL 120
DB 61 GSPPTNLILVDTGSSNFAVGAAHPHPLHRYRQRLSTYRDLRKGVVPTYQKWEGL 120
QY 121 GTDVLVSIHPGPNVTYRANIAATTESDKPFINGSNMGGILGLAYAEIARPDSDLBPFDL 180
DB 121 GTDVLVSIHPGPNVTYRANIAATTESDKPFINGSNMGGILGLAYAEIARPDSDLBPFDL 180
QY 181 VKQTHVPLNLSIQLCGAGFPILNQEVLASVSGSMIIGGIDHSLYTSLWYTPIRREMYE 240
DB 181 VKQTHVPLNLSIQLCGAGFPILNQEVLASVSGSMIIGGIDHSLYTSLWYTPIRREMYE 240
QY 241 VIIIRVEINGODLKMDCKEYNDKSIIVDSGTTNLRPLPKVFEAAVKSIAASTTEKFPDG 300
DB 241 VIIIRVEINGODLKMDCKEYNDKSIIVDSGTTNLRPLPKVFEAAVKSIAASTTEKFPDG 300
QY 301 FWLGEOLVCMQAGTTTWNIFPVISLYLMBEVTNQSFRITILPOQYLRPEVDVATSDDDCY 360
DB 301 FWLGEOLVCMQAGTTTWNIFPVISLYLMBEVTNQSFRITILPOQYLRPEVDVATSDDDCY 360
QY 361 KPFISSSTGTVMGAVIMGFYVVDRAKRIGFVAVSACHVDEFTAAVEGFPVTLDM 420
DB 361 KPFISSSTGTVMGAVIMGFYVVDRAKRIGFVAVSACHVDEFTAAVEGFPVTLDM 420
QY 421 DCGYNIPQTDST 433
DB 421 DCGYNIPQTDST 433

RESULT 5
US-10-281-092-8
/ Sequence 8, Application US/10281092
/ Publication No. US20040121947A1
/ GENERAL INFORMATION:
/ APPLICANT: Ghosh, Arun K.
/ APPLICANT: Tang, Jordan J.N.
/ APPLICANT: Bilec, Geoffrey
/ APPLICANT: Chang, Wenpin
/ APPLICANT: Hong, Lin
/ APPLICANT: Koelsch, Gerald E.
/ APPLICANT: Loy, Jeffrey A.
/ APPLICANT: Turner, Robert T., III

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/ APPLICANT: Devasumadrum, Thippeswamy
/ TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
/ FILE REFERENCE: 2932.1001-004
/ CURRENT APPLICATION NUMBER: US/10/281,092
/ CURRENT FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: US 10/032,818
/ PRIOR FILING DATE: 2001-12-28
/ PRIOR APPLICATION NUMBER: PCT US01/50826
/ PRIOR FILING DATE: 2001-12-28
/ PRIOR APPLICATION NUMBER: US 60/258,705
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: US 60/275,756
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: US 60/335,952
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US 60/333,545
/ PRIOR FILING DATE: 2001-11-27
/ PRIOR APPLICATION NUMBER: US 60/348,464
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/348,615
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/390,804
/ PRIOR FILING DATE: 2002-06-20
/ PRIOR APPLICATION NUMBER: US 60/397,557
/ PRIOR FILING DATE: 2002-07-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 456
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: deduced amino acid sequence of promemapsin 2-T1
/ US-10-281-092-8

Query Match      99.1%; Score 2267; DB 16; Length 456;
Best Local Similarity 99.1%; Pred. No. 5.1e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TOHGRLPLRSGLGAPLGLINLETDEBERPGRGRGSFVEMVDNLRGSGGGYVEMTV 60
DB 24 TOHGRLPLRSGLGAPLGLRLPRETDEBERPGRGRGSFVEMVDNLRGSGGGYVEMTV 83
QY 61 GSPPTNLILVDTGSSNFAVGAAHPHPLHRYRQRLSTYRDLRKGVVPTYQKWEGL 120
DB 61 GSPPTNLILVDTGSSNFAVGAAHPHPLHRYRQRLSTYRDLRKGVVPTYQKWEGL 143
QY 84 GSPPTNLILVDTGSSNFAVGAAHPHPLHRYRQRLSTYRDLRKGVVPTYQKWEGL 143
DB 121 GTDVLVSIHPGPNVTYRANIAATTESDKPFINGSNMGGILGLAYAEIARPDSDLBPFDL 180
QY 144 GTDVLVSIHPGPNVTYRANIAATTESDKPFINGSNMGGILGLAYAEIARPDSDLBPFDL 203
DB 181 VKQTHVPLNLSIQLCGAGFPILNQEVLASVSGSMIIGGIDHSLYTSLWYTPIRREMYE 240
QY 204 VKQTHVPLNLSIQLCGAGFPILNQEVLASVSGSMIIGGIDHSLYTSLWYTPIRREMYE 263
DB 241 VIIIRVEINGODLKMDCKEYNDKSIIVDSGTTNLRPLPKVFEAAVKSIAASTTEKFPDG 300
QY 264 VIIIRVEINGODLKMDCKEYNDKSIIVDSGTTNLRPLPKVFEAAVKSIAASTTEKFPDG 323
DB 301 FWLGEOLVCMQAGTTTWNIFPVISLYLMBEVTNQSFRITILPOQYLRPEVDVATSDDDCY 360
QY 324 FWLGEOLVCMQAGTTTWNIFPVISLYLMBEVTNQSFRITILPOQYLRPEVDVATSDDDCY 383
DB 361 KPFISSSTGTVMGAVIMGFYVVDRAKRIGFVAVSACHVDEFTAAVEGFPVTLDM 420
QY 384 KPFISSSTGTVMGAVIMGFYVVDRAKRIGFVAVSACHVDEFTAAVEGFPVTLDM 443
QY 421 DCGYNIPQTDST 433
DB 444 DCGYNIPQTDST 456

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RESULT 6
US-11-089-918-66
/ Sequence 66, Application US/11089918
/ Publication No. US20050164327A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Basal, Gurigbal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Frigon, Normand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatsuno, Gwen
/ APPLICANT: Tung, Jay
/ APPLICANT: Wang, Shuwen
/ APPLICANT: McConlogue, Lisa
/ TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
/ FILE REFERENCE: 228-US-NEW2C9
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR FILING DATE: 2005-03-25/723,722
/ PRIOR APPLICATION NUMBER: US 09/723,722
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: US 09/471,669
/ PRIOR FILING DATE: 1999-12-24
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 60/139,172
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 66
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-089-918-66

Query Match      99.1%; Score 2267; DB 20; Length 480;
Best Local Similarity 99.1%; Pred. No. 5.5e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TOHGIRLPRLRSGLGAPLGLLEINLETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
DB      1 TOHGIRLPRLRSGLGAPLGLRLPRETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
QY      61 GSPPTLNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVVPYPTQGMKEGL 120
DB      61 GSPPTLNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVVPYPTQGMKEGL 120
QY      121 GTDLVSIPIHGPVNTYRANIAATTESDKPFINSNMEGLIGLAVAIAPDDSLPEFPDL 180
DB      121 GTDLVSIPIHGPVNTYRANIAATTESDKPFINSNMEGLIGLAVAIAPDDSLPEFPDL 180
QY      181 VKQTHVPLNLSIQLCGAGFPLNQSEVLASVSGSMITIGSIDSLVYTGSLMTYPIRREMYE 240
DB      181 VKQTHVPLNLSIQLCGAGFPLNQSEVLASVSGSMITIGSIDSLVYTGSLMTYPIRREMYE 240
QY      241 VTIIVEVEINGODLKNDCKEYNVDKSIIVDSGTTNLRPKKVEEAAVKSIIKAASSTKEKPDG 300
DB      241 VTIIVEVEINGODLKNDCKEYNVDKSIIVDSGTTNLRPKKVEEAAVKSIIKAASSTKEKPDG 300
QY      301 FWLGEOLVCMQAGTTPMNIIPVISLYLMGEVYNOSFRITLIPQOYLRPVEDVATSODDCY 360
DB      301 FWLGEOLVCMQAGTTPMNIIPVISLYLMGEVYNOSFRITLIPQOYLRPVEDVATSODDCY 360
QY      361 KEAIISSQSTGTVMGAVIMEGTYVFDRAKRIIGFAVSAACHVHDEFRTAAVEGPFVTLDME 420
DB      361 KEAIISSQSTGTVMGAVIMEGTYVFDRAKRIIGFAVSAACHVHDEFRTAAVEGPFVTLDME 420
QY      421 DCGYNIPTDEST 433
```

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DB      421 DCGYNIPTDEST 433

RESULT 7
US-11-090-866-66
/ Sequence 66, Application US/11090866
/ Publication No. US20050164294A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Basal, Gurigbal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Frigon, Normand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatsuno, Gwen
/ APPLICANT: Tung, Jay
/ APPLICANT: Wang, Shuwen
/ APPLICANT: McConlogue, Lisa
/ TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
/ FILE REFERENCE: 228-US-NEW2C12
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: US 09/723,722
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: US 09/471,669
/ PRIOR FILING DATE: 1999-12-24
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 60/139,172
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 66
/ LENGTH: 480
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-090-866-66

Query Match      99.1%; Score 2267; DB 20; Length 480;
Best Local Similarity 99.1%; Pred. No. 5.5e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TOHGIRLPRLRSGLGAPLGLLEINLETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
DB      1 TOHGIRLPRLRSGLGAPLGLRLPRETDEPEEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
QY      61 GSPPTLNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVVPYPTQGMKEGL 120
DB      61 GSPPTLNLIVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVVPYPTQGMKEGL 120
QY      121 GTDLVSIPIHGPVNTYRANIAATTESDKPFINSNMEGLIGLAVAIAPDDSLPEFPDL 180
DB      121 GTDLVSIPIHGPVNTYRANIAATTESDKPFINSNMEGLIGLAVAIAPDDSLPEFPDL 180
QY      181 VKQTHVPLNLSIQLCGAGFPLNQSEVLASVSGSMITIGSIDSLVYTGSLMTYPIRREMYE 240
DB      181 VKQTHVPLNLSIQLCGAGFPLNQSEVLASVSGSMITIGSIDSLVYTGSLMTYPIRREMYE 240
QY      241 VTIIVEVEINGODLKNDCKEYNVDKSIIVDSGTTNLRPKKVEEAAVKSIIKAASSTKEKPDG 300
DB      241 VTIIVEVEINGODLKNDCKEYNVDKSIIVDSGTTNLRPKKVEEAAVKSIIKAASSTKEKPDG 300
QY      301 FWLGEOLVCMQAGTTPMNIIPVISLYLMGEVYNOSFRITLIPQOYLRPVEDVATSODDCY 360
DB      301 FWLGEOLVCMQAGTTPMNIIPVISLYLMGEVYNOSFRITLIPQOYLRPVEDVATSODDCY 360
QY      361 KEAIISSQSTGTVMGAVIMEGTYVFDRAKRIIGFAVSAACHVHDEFRTAAVEGPFVTLDME 420
DB      361 KEAIISSQSTGTVMGAVIMEGTYVFDRAKRIIGFAVSAACHVHDEFRTAAVEGPFVTLDME 420
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Db 361 KFAISQSTGTGMAGVIMEGFYVFDPRARKIGFAVSACHVDEFRTAAVEGPFVTLDM 420
Qy 421 DCGYNIPTDEST 433
Db 421 DCGYNIPTDEST 433

RESULT 8
US-11-069-377-66
; Sequence 66, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C8
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-069-377-66

Query Match 99.1%; Score 2267; DB 20; Length 480;
Best Local Similarity 99.1%; Pred. No. 5.5e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TQHGIRLPRLSGAGAPLGLLEINLETDEBEPGRGSGFVEMVDNLRGSGGCIYVEMTV 60
1 TQHGIRLPRLSGAGAPLGLRLPRETDEBEPGRGSGFVEMVDNLRGSGGCIYVEMTV 60
Db 61 GSPPTLNTLIVDTGSSNFVGAAPHPPLHRYQROLSSTYRLRKGVVYVYTGKWEGL 120
61 GSPPTLNTLIVDTGSSNFVGAAPHPPLHRYQROLSSTYRLRKGVVYVYTGKWEGL 120
Qy 121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
Db 121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
Qy 181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
Db 181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
Qy 241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
Db 241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
Qy 301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
Db 301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
Qy 361 KFAISQSTGTGMAGVIMEGFYVFDPRARKIGFAVSACHVDEFRTAAVEGPFVTLDM 420

Db 361 KFAISQSTGTGMAGVIMEGFYVFDPRARKIGFAVSACHVDEFRTAAVEGPFVTLDM 420
Qy 421 DCGYNIPTDEST 433
Db 421 DCGYNIPTDEST 433

RESULT 9
US-11-090-872-66
; Sequence 66, Application US/11090872
; Publication No. US20050177888A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-872-66

Query Match 99.1%; Score 2267; DB 20; Length 480;
Best Local Similarity 99.1%; Pred. No. 5.5e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TQHGIRLPRLSGAGAPLGLLEINLETDEBEPGRGSGFVEMVDNLRGSGGCIYVEMTV 60
1 TQHGIRLPRLSGAGAPLGLRLPRETDEBEPGRGSGFVEMVDNLRGSGGCIYVEMTV 60
Db 61 GSPPTLNTLIVDTGSSNFVGAAPHPPLHRYQROLSSTYRLRKGVVYVYTGKWEGL 120
61 GSPPTLNTLIVDTGSSNFVGAAPHPPLHRYQROLSSTYRLRKGVVYVYTGKWEGL 120
Qy 121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
Db 121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
121 GTDLVSIPIHGPNTVYRANIAITTESDKPFINGSNMEGILGLAYAEIARPDSDLPEPFDL 180
Qy 181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
Db 181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
181 VKQTHVPNLFSIQLCGAGFPLNQSEVLASVSGSMITGGIDHSLYTGSLMTYTPIRREWYE 240
Qy 241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
Db 241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
241 VTIIVREINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKFPDG 300
Qy 301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
Db 301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360
301 FMIGBOLVCMQAGTTPWNIIPVYISLYLMGEVTNOSFRITILPOOYLRPVEDVATSODDCY 360

Db 301 FWLGEOLVQWQAGTTPMNIFFVISLYLMEVNTQSFRTITLIPQOYLRPVEDVATSDDCY 360
QY 361 KFAISQSTGTVMGAVINEGFYVFDRAKRRIGFAVSACHVHDEFRTAAVEGPFVTLTDM 420
Db 361 KFAISQSTGTVMGAVINEGFYVFDRAKRRIGFAVSACHVHDEFRTAAVEGPFVTLTDM 420
QY 421 DCGYNIPTDEST 433
Db 421 DCGYNIPTDEST 433

RESULT 10
US-09-796-264-2
; Sequence 2, Application US/09796264
; Patent No. US20020049303A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRP 179
; CURRENT APPLICATION NUMBER: US/09/796,264
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Purified Memapsin 2
; OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
; OTHER INFORMATION: residues
; OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
; OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and
; OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
; OTHER INFORMATION: inhibitor
; OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
; OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
; OTHER INFORMATION: 220-224 are N-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
; OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
; OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
; OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
; OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
; OTHER INFORMATION: and 427-431 are C-lobe Helices
; US-09-796-264-2

Query Match 99.1%; Score 2267; DB 9; Length 488;
Best Local Similarity 99.1%; Pred No. 5,6e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TOHGIRLRPLRSGAGAPLGLINLETDEPEBPGRGSFVEMVNLKSGSGQGYVEMTV 60
Db 9 TOHGIRLRPLRSGAGAPLGLRPRETDEPEBPGRGSFVEMVNLKSGSGQGYVEMTV 68
QY 61 GSPPTLNIIVDTGSSNFAVGAAPRPFHRRYQQLSTTYDLDKGYVVPYTGKWEGL 120
Db 69 GSPPTLNIIVDTGSSNFAVGAAPRPFHRRYQQLSTTYDLDKGYVVPYTGKWEGL 128
QY 121 GTDLVSIPIHGNVTVRANIAAITSDKFFINGSNWEGILGLAVALIAPDPSLEPPDSL 180

Db 129 GTDLVSIPIHGNVTVRANIAAITSDKFFINGSNWEGILGLAVALIAPDPSLEPPDSL 188
QY 181 VQOTHPNLFSLQCGAGFPLNQSIVLASVCGSMITGIDHSYLTGSLMYTPIRREWYE 240
Db 189 VQOTHPNLFSLQCGAGFPLNQSIVLASVCGSMITGIDHSYLTGSLMYTPIRREWYE 248
QY 241 VILIRVEINGODLKMDCKEYNYDKSIYDSGTTNLRPKVVEAAVKSISKASSTEKPPDG 300
Db 249 VILIRVEINGODLKMDCKEYNYDKSIYDSGTTNLRPKVVEAAVKSISKASSTEKPPDG 308
QY 301 FWLGEOLVQWQAGTTPMNIFFVISLYLMEVNTQSFRTITLIPQOYLRPVEDVATSDDCY 360
Db 309 FWLGEOLVQWQAGTTPMNIFFVISLYLMEVNTQSFRTITLIPQOYLRPVEDVATSDDCY 368
QY 361 KFAISQSTGTVMGAVINEGFYVFDRAKRRIGFAVSACHVHDEFRTAAVEGPFVTLTDM 420
Db 369 KFAISQSTGTVMGAVINEGFYVFDRAKRRIGFAVSACHVHDEFRTAAVEGPFVTLTDM 428
QY 421 DCGYNIPTDEST 433
Db 429 DCGYNIPTDEST 441

RESULT 11
US-09-845-226-2
; Sequence 2, Application US/09845226
; Patent No. US20020115600A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Hong, Lin
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: OMRP 182
; CURRENT APPLICATION NUMBER: US/09/845,226
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/603,713
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Purified Memapsin 2
; OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
; OTHER INFORMATION: residues
; OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
; OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and
; OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
; OTHER INFORMATION: inhibitor
; OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
; OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
; OTHER INFORMATION: 220-224 are N-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
; OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
; OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
; OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
; OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
; OTHER INFORMATION: and 427-431 are C-lobe Helices
; US-09-845-226-2

Query Match 99.1%; Score 2267; DB 9; Length 488;

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Best Local Similarity 99.1%; Pred. No. 5,6e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TOHGIRLPLRSGLGAPGLGRLINLETDEEPEEPRGRSGFVEMVDNLRGSGGGYVEMTV 60
DB 9 TQHGIRLPLRSGLGAPGLGRLINLETDEEPEEPRGRSGFVEMVDNLRGSGGGYVEMTV 68
QY 61 GSPPTLNLVDTGSSNFVGAAPHPFLHRYQRLSSTYRDLRKGVVPTQKMEGEL 120
DB 69 GSPPTLNLVDTGSSNFVGAAPHPFLHRYQRLSSTYRDLRKGVVPTQKMEGEL 128
QY 121 GTDIVSIPHPGPNVTVRANIAATTESDKFFINSNMEGILGLAYAEIARPDLSLEPPDSL 180
DB 129 GTDIVSIPHPGPNVTVRANIAATTESDKFFINSNMEGILGLAYAEIARPDLSLEPPDSL 188
QY 181 VKQTHVPLNLSQLCGAGFPLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 240
DB 189 VKQTHVPLNLSQLCGAGFPLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 248
QY 241 VTIIRVEINGODLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSITAASTTEKFPDG 300
DB 249 VTIIRVEINGODLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSITAASTTEKFPDG 308
QY 301 FWMGEOLVCMQAGTTPMNIFPVISLYLMEGVNOSFRITLLPOQYLRPEVDATSDDDCY 360
DB 309 FWMGEOLVCMQAGTTPMNIFPVISLYLMEGVNOSFRITLLPOQYLRPEVDATSDDDCY 368
QY 361 KPAISOSTGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFTAAVEGFPVTLDM 420
DB 369 KPAISOSTGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFTAAVEGFPVTLDM 428
QY 421 DCGYNIPQTEEST 433
DB 429 DCGYNIPQTEEST 441

RESULT 12
US-09-795-903A-2
; Sequence 2, Application US/09795903A
; Patent No. US20020164760A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xindi
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMRP 179
; CURRENT APPLICATION NUMBER: US/09/795,903A
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Purified Memapsin 2
; OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
; OTHER INFORMATION: residues
; OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
; OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and
; OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
; OTHER INFORMATION: inhibitor

```

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; OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
; OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
; OTHER INFORMATION: 220-224 are N-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
; OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
; OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
; OTHER INFORMATION: 354-357, 372-375, 380-383, 390-395,
; OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
; OTHER INFORMATION: and 427-431 are C-lobe Helices
; US-09-795-903A-2

Query Match 99.1%; Score 2267; DB 9; Length 488;
Best Local Similarity 99.1%; Pred. No. 5,6e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TOHGIRLPLRSGLGAPGLGRLINLETDEEPEEPRGRSGFVEMVDNLRGSGGGYVEMTV 60
DB 9 TQHGIRLPLRSGLGAPGLGRLINLETDEEPEEPRGRSGFVEMVDNLRGSGGGYVEMTV 68
QY 61 GSPPTLNLVDTGSSNFVGAAPHPFLHRYQRLSSTYRDLRKGVVPTQKMEGEL 120
DB 69 GSPPTLNLVDTGSSNFVGAAPHPFLHRYQRLSSTYRDLRKGVVPTQKMEGEL 128
QY 121 GTDIVSIPHPGPNVTVRANIAATTESDKFFINSNMEGILGLAYAEIARPDLSLEPPDSL 180
DB 129 GTDIVSIPHPGPNVTVRANIAATTESDKFFINSNMEGILGLAYAEIARPDLSLEPPDSL 188
QY 181 VKQTHVPLNLSQLCGAGFPLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 240
DB 189 VKQTHVPLNLSQLCGAGFPLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 248
QY 241 VTIIRVEINGODLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSITAASTTEKFPDG 300
DB 249 VTIIRVEINGODLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSITAASTTEKFPDG 308
QY 301 FWMGEOLVCMQAGTTPMNIFPVISLYLMEGVNOSFRITLLPOQYLRPEVDATSDDDCY 360
DB 309 FWMGEOLVCMQAGTTPMNIFPVISLYLMEGVNOSFRITLLPOQYLRPEVDATSDDDCY 368
QY 361 KPAISOSTGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFTAAVEGFPVTLDM 420
DB 369 KPAISOSTGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFTAAVEGFPVTLDM 428
QY 421 DCGYNIPQTEEST 433
DB 429 DCGYNIPQTEEST 441

RESULT 13
US-10-032-818-2
; Sequence 2, Application US/10032818
; Publication No. US20030092629A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Koelsch, Gerald
; APPLICANT: Ghosh, Arun K.
; TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
; FILE REFERENCE: 2932.1006-007
; CURRENT APPLICATION NUMBER: US/10/032,818
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/275,756
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 60/258,705
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-032-818-2

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Query Match 99.1%; Score 2267; DB 14; Length 488;
Best Local Similarity 99.1%; Pred. No. 5.6e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TQHGIRLPRLRSGLGAPLGLEINLETDEEPEERGRSGFVEMVDNLKSGGQGYVEMTV 60
DB 9 TQHGIRLPRLRSGLGAPLGRLPRETDEEPEERGRSGFVEMVDNLKSGGQGYVEMTV 68
QY 61 GSPQTNIILVDTGSSNFAVGAAPHPLHRYORQLSSTRDLRKGYVYVYTGKMEGEL 120
DB 69 GSPQTNIILVDTGSSNFAVGAAPHPLHRYORQLSSTRDLRKGYVYVYTGKMEGEL 128
QY 121 GTDLVSIIPHGNVTVRANIAITSDKPFINGSNWEGILGLAYAEIARPPDSLEPPDSL 180
DB 129 GTDLVSIIPHGNVTVRANIAITSDKPFINGSNWEGILGLAYAEIARPPDSLEPPDSL 188
QY 181 VKQTHVNLFSLOLCGAGFPLNOSVLA SVGSMITIGIDHSLYTSGLMWTPRRRMYE 240
DB 189 VKQTHVNLFSLOLCGAGFPLNOSVLA SVGSMITIGIDHSLYTSGLMWTPRRRMYE 248
QY 241 VIIVRVINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIAASTKPEPDG 300
DB 249 VIIVRVINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIAASTKPEPDG 308
QY 301 FMIGEOLVCMQAGTTPNIPVVISLYMGEVTVNQSFRITLLPQOYLRPVEDVATSDDCY 360
DB 309 FMIGEOLVCMQAGTTPNIPVVISLYMGEVTVNQSFRITLLPQOYLRPVEDVATSDDCY 368
QY 361 KFAISGSSTGTWGAIVMEGFYVFPDRAKRIGFASACHVDEFTAAVEGPFVTLME 420
DB 369 KFAISGSSTGTWGAIVMEGFYVFPDRAKRIGFASACHVDEFTAAVEGPFVTLME 428
QY 421 DCGYNIPQTDST 433
DB 429 DCGYNIPQTDST 441

RESULT 14
US-10-820-953-2
Sequence 2, Application US/10820953
Publication No. US20040167075A1
GENERAL INFORMATION:
APPLICANT: Tang, Jordan J.N.
APPLICANT: Hong, Lin
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: OMRP 182
CURRENT APPLICATION NUMBER: US/10/820,953
PRIOR APPLICATION NUMBER: US/09/603,713
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: 60/141,363
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 60/178,368
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/210,292
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 488
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Purified Memapsin 2
OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
OTHER INFORMATION: Residues
OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and

OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
OTHER INFORMATION: Inhibitor
OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
OTHER INFORMATION: 220-224 are N-lobe Beta Strands
OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 364-387,
OTHER INFORMATION: and 427-431 are C-lobe Helices
US-10-820-953-2

Query Match 99.1%; Score 2267; DB 16; Length 488;
Best Local Similarity 99.1%; Pred. No. 5.6e-209;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TQHGIRLPRLRSGLGAPLGLEINLETDEEPEERGRSGFVEMVDNLKSGGQGYVEMTV 60
DB 9 TQHGIRLPRLRSGLGAPLGRLPRETDEEPEERGRSGFVEMVDNLKSGGQGYVEMTV 68
QY 61 GSPQTNIILVDTGSSNFAVGAAPHPLHRYORQLSSTRDLRKGYVYVYTGKMEGEL 120
DB 69 GSPQTNIILVDTGSSNFAVGAAPHPLHRYORQLSSTRDLRKGYVYVYTGKMEGEL 128
QY 121 GTDLVSIIPHGNVTVRANIAITSDKPFINGSNWEGILGLAYAEIARPPDSLEPPDSL 180
DB 129 GTDLVSIIPHGNVTVRANIAITSDKPFINGSNWEGILGLAYAEIARPPDSLEPPDSL 188
QY 181 VKQTHVNLFSLOLCGAGFPLNOSVLA SVGSMITIGIDHSLYTSGLMWTPRRRMYE 240
DB 189 VKQTHVNLFSLOLCGAGFPLNOSVLA SVGSMITIGIDHSLYTSGLMWTPRRRMYE 248
QY 241 VIIVRVINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIAASTKPEPDG 300
DB 249 VIIVRVINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIAASTKPEPDG 308
QY 301 FMIGEOLVCMQAGTTPNIPVVISLYMGEVTVNQSFRITLLPQOYLRPVEDVATSDDCY 360
DB 309 FMIGEOLVCMQAGTTPNIPVVISLYMGEVTVNQSFRITLLPQOYLRPVEDVATSDDCY 368
QY 361 KFAISGSSTGTWGAIVMEGFYVFPDRAKRIGFASACHVDEFTAAVEGPFVTLME 420
DB 369 KFAISGSSTGTWGAIVMEGFYVFPDRAKRIGFASACHVDEFTAAVEGPFVTLME 428
QY 421 DCGYNIPQTDST 433
DB 429 DCGYNIPQTDST 441

RESULT 15
US-10-773-754-2
Sequence 2, Application US/10773754
Publication No. US20040220079A1
GENERAL INFORMATION:
APPLICANT: Koelsch, Gerald
APPLICANT: Tang, Jordan J. N.
APPLICANT: Hong, Lin
APPLICANT: Ghosh, Arun K.
TITLE OF INVENTION: The Board of Trustees of the University of Illinois
TITLE OF INVENTION: Inhibitors of Memapsin 2 and Use Thereof
FILE REFERENCE: 022266-000930US
CURRENT APPLICATION NUMBER: US/10/773,754
PRIOR FILING DATE: 2004-02-06
PRIOR APPLICATION NUMBER: US 60/141,363
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 60/168,060
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: US 60/177,836
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 60/178,368

;; PRIOR FILING DATE: 2000-01-27
;; PRIOR APPLICATION NUMBER: US 60/210,292
;; PRIOR FILING DATE: 2000-06-08
;; PRIOR APPLICATION NUMBER: US 09/603,713
;; PRIOR FILING DATE: 2000-06-27
;; PRIOR APPLICATION NUMBER: US 09/645,226
;; PRIOR FILING DATE: 2001-04-30
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 488
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: purified memapsin 2, aspartic proteainase 2 (ASP2)
;; FEATURE:
;; OTHER INFORMATION: amino acids 28-48 are remnant putative propeptide
;; FEATURE:
;; OTHER INFORMATION: residues
;; FEATURE:
;; OTHER INFORMATION: amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
;; OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
;; OTHER INFORMATION: 220-224 are N-lobe beta strands
;; FEATURE:
;; OTHER INFORMATION: amino acids 58-61, 78, 80, 82-83, 116, 118-121,
;; OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and
;; OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
;; OTHER INFORMATION: inhibitor
;; FEATURE:
;; OTHER INFORMATION: amino acids 184-191 and 210-217 are N-lobe helices
;; FEATURE:
;; OTHER INFORMATION: amino acids 237-240, 247-249, 251-256, 259-260,
;; OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
;; OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
;; OTHER INFORMATION: 400-405, and 418-420 are C-lobe beta strands
;; FEATURE:
;; OTHER INFORMATION: amino acids 286-299, 307-310, 350-353, 384-387,
;; OTHER INFORMATION: and 427-431 are C-lobe helices
;; US-10-773-754-2

Query Match 99.1%; Score 2267; DB 16; Length 488;
Best Local Similarity 99.1%; Pred. No. 5,66-209;

Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TQHGRLPLRSGLGAPLGLEINLETDPEBEPGRGSPVEMVDNLKSGSGGYVEMTV 60
DB 9 TQHGRLPLRSGLGAPLGRLPRETDEBEPGRGSPVEMVDNLKSGSGGYVEMTV 68
QY 61 GSPPTLNLIVDTGSSNFAVGAAPHPPLHRYRQRLSSTYRDLRKGVYVYTGKWEGL 120
DB 69 GSPPTLNLIVDTGSSNFAVGAAPHPPLHRYRQRLSSTYRDLRKGVYVYTGKWEGL 128
QY 121 GTPLVSLPHGPNTVAVANIAITESDKEPFIINGSNWEGILGLAYAEIARPPDSL 180
DB 129 GTPLVSLPHGPNTVAVANIAITESDKEPFIINGSNWEGILGLAYAEIARPPDSL 188
QY 181 VKQTHVNLFSLOLCGAFPLNOSVLAASVGSNIIIGIDHSLYTGSLWYTPIRREWEY 240
DB 189 VKQTHVNLFSLOLCGAFPLNOSVLAASVGSNIIIGIDHSLYTGSLWYTPIRREWEY 248
QY 241 VILVVEINQDLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKEFPDG 300
DB 249 VILVVEINQDLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTKEFPDG 308
QY 301 FMIQEOLVCMQAGTTPNIPVLSLYMGEVNSFRITLPOOYLRPVEDVATSODDCY 360
DB 309 FMIQEOLVCMQAGTTPNIPVLSLYMGEVNSFRITLPOOYLRPVEDVATSODDCY 368
QY 361 KPAISGSSTGTWGAIVMEGFYVFDRAKRIQPAVSACHVHDEFRTAAVEGPPVTLME 420
DB 369 KPAISGSSTGTWGAIVMEGFYVFDRAKRIQPAVSACHVHDEFRTAAVEGPPVTLME 428
QY 421 DCGYNIPQTEST 433
|||||

DB 429 DCGYNIPQTEST 441

Search completed: August 22, 2005, 00:54:04
Job time : 1528 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 21, 2005, 06:58:03 ; Search time 125 Seconds
(without alignments)
1339.738 Million cell updates/sec

Title: US-10-726-967A-84

Sequence: 1 TQHGIRLPLRSGLGAPLGL.....FVTLDMEDCGYNIPTDEST 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

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Database :
A: Geneseqp_16dec04:*
1:  Geneseqqp1980s:*
2:  Geneseqqp1990s:*
3:  Geneseqqp2000s:*
4:  Geneseqqp2001s:*
5:  Geneseqqp2002s:*
6:  Geneseqqp2003as:*
7:  Geneseqqp2003bs:*
8:  Geneseqqp2004as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2288	100.0	433	8	ADP83957	Adp83957 Human BAC
2	2286	99.9	433	8	ADP83954	Adp83954 Human BAC
3	2273	99.3	433	8	ADP83951	Adp83951 Human BAC
4	2267	99.1	435	8	ADP66641	Adi66641 Mature hu
5	2267	99.1	456	8	ABR61929	Abt61929 Human pro
6	2267	99.1	488	4	AAB61334	Aab61334 Wemapsin
7	2267	99.1	488	4	AAB66572	Aab66572 Human mem
8	2267	99.1	488	5	ABG78372	Abg78372 Human pro
9	2267	99.1	488	5	AAU99488	Aau99488 Human mem
10	2267	99.1	488	6	ABG76101	Abg76101 Human par
11	2267	99.1	488	6	ADA74817	Ada74817 Human mem
12	2267	99.1	501	3	AA94767	Human Det
13	2267	99.1	501	3	ABB07896	Aab07896 Amino acil
14	2267	99.1	501	5	ABG78374	Human pre37
15	2267	99.1	501	6	ABR61928	Abtr61928 Human mem
16	2267	99.1	501	7	ADLC81560	Adc81560 Human BAC
17	2267	99.1	501	7	ADL18184	Adl18184 Human APP
18	2267	99.1	501	8	ADG686751	Adg686751 Human APP
19	2267	99.1	501	8	ADU94316	Adj94316 Human assp
20	2267	99.1	501	8	AD050412	Ado50412 Human assp
21	2267	99.1	501	8	ADQ17468	Adq17468 Human sof
22	2267	99.1	501	8	ADP83876	Adp83876 Human BAC
23	2267	99.1	501	8	ADR75325	Adr75325 Human assp
24	2267	99.1	503	4	ABB61335	Aab61335 T7 promot
25	2267	99.1	503	4	AAB66573	Aab66573 Human pro

26	2267	99.1	503	5	ABG78373	Human p
27	2267	99.1	503	5	AAU99489	Pro-nem
28	2267	99.1	503	6	ABG76102	Human mem
29	2267	99.1	503	6	AAW52697	AdA7818
30	2267	99.1	509	5	AAW52697	FLAG-cag
31	2267	99.1	509	8	ADJ71858	Human pro
32	2267	99.1	509	8	ADP74535	Human ind
33	2262	98.9	453	3	AAW89438	Modifed
34	2262	98.9	453	3	AAU07215	Human asp
35	2262	98.9	453	4	AAU10642	Human-Asp
36	2262	98.9	453	4	AAE06872	Human-Asp
37	2262	98.9	453	4	AAE02594	Human-Asp
38	2262	98.9	453	4	AAU06616	Human-Asp
39	2262	98.9	453	5	ABW78603	Human Asp
40	2262	98.9	453	8	ADJ94542	Human-p
41	2262	98.9	453	8	ADU50438	Human Asp
42	2262	98.9	453	8	ADU55351	Human Asp
43	2262	98.9	455	8	ADU57773	BACE WT p
44	2262	98.9	459	3	AAW88439	Modifed
45	2262	98.9	459	4	AAU07216	Human asp

ALIGNMENTS

RESULT 1
ADP83957
ID ADP83957 standard; protein; 433 AA

AC	ADP83957;	
XX		
DT	23-SEP-2004	(first entry)
XX		
DE	Human BACE1 mutant amino acid sequence SEQ ID NO: 84	

KM human; beta-site amyloid precursor protein cleaving enzyme 1;
KM beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; chromosome 11
KM prodomain; engineered cleavage site; protease domain; neuroprotective;
KM neurotropic; gene therapy; Alzheimer's disease; Down's syndrome; mutant.

OS	Homo sapiens.
OS	Synthetic.

PN WO2004056962-A2

PD 08-JUL-2004.

PF 02-DEC-2003; 2003WO-US038314

PR 04-DEC-2002; 2002US-0430984P

PA (SUNE-) SUNESIS PHARM INC.

PI Ballinger M;

DR WPI; 2004-507703/48.

PT New polypeptides for producing homogenously processed preparations of
PT beta site amyloid precursor protein-cleaving enzyme comprises a
PT prodomain, an engineered cleavage site and a protease domain.

PS Example 1; SEQ ID NO 84; 40pp; English.

The present invention describes a polypeptide (1) comprising in order from the N-terminus to the C-terminus: (a) a prodomain comprising at least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID NO:3 (ADP81877), comprising residues 22-37 of SEQ ID NO:1 (ADP63876) which is the largest isoform of human beta-site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1), isoform A); (b) an engineered cleavage site; and (c) a protease domain. (1) is capable of being cleaved at the engineered cleavage site, and so releases a free protease domain that has BACE1 activity. Also described: (1) a nucleic acid sequence encoding (1). (2) a vector for expression of (1), and (3) a host cell expressing (1).

CC (I) has neuroprotective and nootropic activities, and can be used in gene
CC therapy. (I) can be used for producing preparations of homogenously
CC processed BACE that may be used for e.g. studying or treating diseases
CC such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is
CC located on chromosome 11, more specifically to 11q23.2-23.3. The present
CC sequence represents a mutant human BACE1 amino acid sequence, which is
CC used in an example from the present invention.

XX Sequence 433 AA;

Query Match 100.0%; Score 2288; DB 8; Length 433;
Best Local Similarity 100.0%; Pred. No. 6, 6e-216;
Matches 433; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TQHGIRLPRLRSGLGAPLGLGELINLETDEBEPEGRGSEVEMVDNLRKSGGGGYEMTV 60
    |||||
DB 1 TQHGIRLPRLRSGLGAPLGLGELINLETDEBEPEGRGSEVEMVDNLRKSGGGGYEMTV 60
QY 61 GSPPTNLINLVDTGSSNFAYGAPHPFLHRYRORLSTYRDLRKGVVYPYTGKWEGL 120
    |||||
DB 61 GSPPTNLINLVDTGSSNFAYGAPHPFLHRYRORLSTYRDLRKGVVYPYTGKWEGL 120
QY 121 GTDLVSIPIHGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
    |||||
DB 121 GTDLVSIPIHGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
QY 181 VKQTHVNLFSIQLCGAGFPPLNOSVLAIVGSMITIGIDHSLYTGSMTYPIRREWYE 240
    |||||
DB 181 VKQTHVNLFSIQLCGAGFPPLNOSVLAIVGSMITIGIDHSLYTGSMTYPIRREWYE 240
QY 241 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTNLRPKKVFEEAIVSIKAASTKFPDG 300
    |||||
DB 241 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTNLRPKKVFEEAIVSIKAASTKFPDG 300
QY 301 FMIAGEOLVCMQAGTTPMNIFFPVISLYLMEVTNOSFRITTLPOQYLARVEDVATSQDDCY 360
    |||||
DB 301 FMIAGEOLVCMQAGTTPMNIFFPVISLYLMEVTNOSFRITTLPOQYLARVEDVATSQDDCY 360
QY 361 KFAISQSSGTGTMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFRITAAVSGPFTLME 420
    |||||
DB 361 KFAISQSSGTGTMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFRITAAVSGPFTLME 420
QY 421 DCGYNIPQTDSEST 433
    |||||
DB 421 DCGYNIPQTDSEST 433
```

RESULT 2
ADP83954
ID ADP83954 standard; protein; 433 AA.
XX
AC ADP83954;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human BACE1 mutant amino acid sequence SEQ ID NO:81.
XX
KW human; beta-site amyloid precursor protein cleaving enzyme 1;
KW beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; chromosome 11;
KW prodomain; engineered cleavage site; protease domain; neuroprotective;
KW nootropic; gene therapy; Alzheimer's disease; Down's syndrome; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004056962-A2.
XX
PD 08-JUL-2004.
XX
PF 02-DEC-2003; 2003WO-US038314.
XX
PR 04-DEC-2002; 2002US-0430984P.
XX

PA (SUNE-) SUNESIS PHARM INC.
XX
XX Ballinger M;
XX
DR WPI, 2004-507703/48.

PT New polypeptides for producing homogenously processed preparations of
PT beta site amyloid precursor protein-cleaving enzyme comprises a
PT prodomain, an engineered cleavage site and a protease domain.
XX
XX Example 1; SEQ ID NO 81; 40pp; English.

CC The present invention describes a polypeptide (I) comprising in order
CC from the N-terminus to the C-terminus: (a) a prodomain comprising at
CC least 6 contiguous amino acids of the 16 amino acid sequence of SEQ ID
CC NO:3 (ADP83877), comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which
CC is the longest isoform of human beta-site amyloid precursor protein (APP)
CC cleaving enzyme 1 (BACE1), (isoform A); (b) an engineered cleavage site;
CC and (c) a protease domain. (I) is capable of being cleaved at the
CC engineered cleavage site, and so releases a free protease domain that has
CC BACE1 activity. Also described: (1) a nucleic acid sequence encoding (I);
CC (2) a vector for expression of (I); and (3) a host cell expressing (I).
CC (I) has neuroprotective and nootropic activities, and can be used in gene
CC therapy. (I) can be used for producing preparations of homogenously
CC processed BACE that may be used for e.g. studying or treating diseases
CC such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is
CC located on chromosome 11, more specifically to 11q23.2-23.3. The present
CC sequence represents a mutant human BACE1 amino acid sequence, which is
CC used in an example from the present invention.

XX Sequence 433 AA;

Query Match 99.9%; Score 2286; DB 8; Length 433;
Best Local Similarity 99.8%; Pred. No. 1e-215;
Matches 432; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TQHGIRLPRLRSGLGAPLGLGELINLETDEBEPEGRGSEVEMVDNLRKSGGGGYEMTV 60
    |||||
DB 1 TQHGIRLPRLRSGLGAPLGLGELINLETDEBEPEGRGSEVEMVDNLRKSGGGGYEMTV 60
QY 61 GSPPTNLINLVDTGSSNFAYGAPHPFLHRYRORLSTYRDLRKGVVYPYTGKWEGL 120
    |||||
DB 61 GSPPTNLINLVDTGSSNFAYGAPHPFLHRYRORLSTYRDLRKGVVYPYTGKWEGL 120
QY 121 GTDLVSIPIHGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
    |||||
DB 121 GTDLVSIPIHGPNVTVRANIAAITESDKFFINGSNMEGILGLAYAEIARPDLSLEPPFDSL 180
QY 181 VKQTHVNLFSIQLCGAGFPPLNOSVLAIVGSMITIGIDHSLYTGSMTYPIRREWYE 240
    |||||
DB 181 VKQTHVNLFSIQLCGAGFPPLNOSVLAIVGSMITIGIDHSLYTGSMTYPIRREWYE 240
QY 241 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTNLRPKKVFEEAIVSIKAASTKFPDG 300
    |||||
DB 241 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTNLRPKKVFEEAIVSIKAASTKFPDG 300
QY 301 FMIAGEOLVCMQAGTTPMNIFFPVISLYLMEVTNOSFRITTLPOQYLARVEDVATSQDDCY 360
    |||||
DB 301 FMIAGEOLVCMQAGTTPMNIFFPVISLYLMEVTNOSFRITTLPOQYLARVEDVATSQDDCY 360
QY 361 KFAISQSSGTGTMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFRITAAVSGPFTLME 420
    |||||
DB 361 KFAISQSSGTGTMGAVIMEGFYVFPDRARKRIGFAVSACHVDEFRITAAVSGPFTLME 420
QY 421 DCGYNIPQTDSEST 433
    |||||
DB 421 DCGYNIPQTDSEST 433
```

RESULT 3
ADP83951
ID ADP83951 standard; protein; 433 AA.
XX

AC	ADP83951;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	Human BACE1 mutant amino acid sequence SEQ ID NO:78.
XX	
KW	human; beta-site amyloid precursor protein cleaving enzyme 1;
KW	beta-site APP cleaving enzyme 1; BACE1; BACE1 isoform A; chromosome 11;
KW	prodomain; engineered cleavage site; protease domain; neuroprotective;
KW	neurotropic; gene therapy; Alzheimer's disease; Down's syndrome; mutant.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO2004056962-A2.
XX	
PD	08-JUL-2004.
XX	
PF	02-DEC-2003; 2003WO-US038314.
XX	
PR	04-DEC-2002; 2002US-0430984P.
XX	
PA	(SUNE-) SUNEIS PHARM INC.
XX	
PI	Ballinger M;
XX	
DR	WPI; 2004-507703/48.
XX	
PT	New polypeptides for producing homogeneously processed preparations of
PT	beta site amyloid precursor protein-cleaving enzyme comprises a
PT	prodomain, an engineered cleavage site and a protease domain.
XX	
XX	Example 1; SEQ ID NO 78; 40pp; English.

The present invention describes a polypeptide (1) comprising in order from the N-terminus to the C-terminus: (a) a prodomain sequence of SEQ ID NO:3 (ADP83877), comprising residues 22-37 of SEQ ID NO:1 (ADP83876) which is the longest isoform of human beta-site amyloid precursor protein (APP) cleaving enzyme 1 (BACE1), isoform A); (b) an engineered cleavage site; and (c) a protease domain. (1) is capable of being cleaved at the engineered cleavage site, and so releases a free protease domain that has BACE1 activity. Also described: (1) a nucleic acid sequence encoding (1); (2) a vector for expression of (1); and (3) a host cell expressing (1). (1) has neuroprotective and neurotropic activities, and can be used in gene therapy. (1) can be used for producing preparations of homogeneously processed BACE that may be used for e.g. studying or treating diseases such as Alzheimer's disease or Down's syndrome. The human BACE1 gene is located on chromosome 11, more specifically to 11q23.2-23.3. The present sequence represents a mutant human BACE1 amino acid sequence, which is used in an example from the present invention.

Query Match	99.3%	Score 2273	DB 8	Length 433
Best Local Similarity	99.3%	Pred. No. 2e-214		
Matches 430; Conservative	1	Mismatches 2	Indels 0	Gaps 0

QY	1	TOHGILPRSGGAGAPLGLEINLEFDEDEEGRGSGSEVEMWMDNRGSGGQYVEMTV	60
Db	1	TOHGIRLPFRSGGAGAPLGRLPLEFDEDEEGRGSGSEVEMWMDNRGSGGQYVEMTV	60
QY	61	GSPPQTLLIVDTGSSNFAVGAAPHFPLHRYQROLSTFYRLRKGVVYPYTGKMEGL	120
Db	61	GSPPQTLLIVDTGSSNFAVGAAPHFLHRYQROLSTFYRLRKGVVYPYTGKMEGL	120
QY	121	GTDLVSI PHGPNVTVAANIAITESQKFFINSGNMEGILGLAYAEIARPDDSLAEPPDGL	180
Db	121	GTDLVSI PHGPNVTVAANIAITESQKFFINSGNMEGILGLAYAEIARPDDSLAEPPDGL	180
QY	181	VKQTHVNNFLSLOLCGAGPPLNSEVLAIVSGSMIIIGIDHSLYTSLSWVTPPIRRMEVYE	240
Db	181	VKQTHVNNFLSLOLCGAGPPLNSEVLAIVSGSMIIIGIDHSLYTSLSWVTPPIRRMEVYE	240

QY	241	VIIIVREINIGOLIKRDCCEXYNDKSIYDSGTTNLRLEPKYFEAAVKSIIKAASSTKRPDC	300
QY	241	VIIIVREINIGOLIKRDCCEXYNDKSIYDSGTTNLRLEPKYFEAAVKSIIKAASSTKRPDC	300
Db	241	VIIIVREINIGOLIKRDCCEXYNDKSIYDSGTTNLRLEPKYFEAAVKSIIKAASSTKRPDC	300
QY	301	FMLGEOLVCMOAGTTPMNI.FPVI.SLYLMGEVYTNOSFRITTL.PQOYL.RPVEDVATSODCY	360
Db	301	FMLGEOLVCMOAGTTPMNI.FPVI.SLYLMGEVYTNOSFRITTL.PQOYL.RPVEDVATSODCY	360
QY	361	KPAISOSSTGTTMGAVINIEGFVYVVDRAKRI.GPAVNSACHHDEF.RPAALVEG.PVTLTME	420
Db	361	KPAISOSSTGTTMGAVINIEGFVYVVDRAKRI.GPAVNSACHHDEF.RPAALVEG.PVTLTME	420
QY	421	DCGYNI.POTDEST	433
Db	421	DCGYNI.POTDEST	433

RESULT 4
ADI64641
ID ADI64641 standard; protein; 435 AA

AC ADI64641;

DT 22-APR-2004 (first entry)

DE Mature human pro-beta-secretase (pro-BACE) protein seq id 2.

KM crystal; glycosylated human beta-secretase; BACE; human beta-secretase
KM protein co-ordinate data; pro-BACE.
KM

Homo sapiens.

PN US2004014194-A1.

PD 22-JAN-2004.

PF 26-MAR-2003; 2003US-00400273.

27-MAR-2002; 2002US-0367937P.

PA (SCHE) SCHERING CORP.

PI Bever BM, Hammond GS,

[illegible]

WFL; 2004-10/320/10-
DK
XX

PT New crystal comprising a group of useful for determining the

PT and other related proteins.

PS CLAIM 15; SEQ ID NO 2; 10/PP; ENGLISH
XY

CC The invention de
CC secretase polym

CC a root mean square
CC than 1.5 Angstroms

CC structural coord
CC dimensional] stru

CC is the amino acid

SQ Sequence 435 AA;

Query Match
Post 1000] Similar

Matches 429; Cons

QY 1 TQHGIRL

Db 1 TONGIRI

QY 61 GSPPQTL

[illegible]

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Db 61 GSPPTQTLNIIIVDTSSNFAVGAPFLHRYRQQLSTYRDLKKGYYVPTTQKMEGEL 120
QY 121 GTDLVSIHFGPNVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPDSTL 180
Db 121 GTDLVSIHFGPNVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPDSTL 180
QY 181 VKQTHVPLFSLQCGAGFPLNQGSEVLASVGSMTIGIDHSLYTGSLSWYTPIRREYYE 240
Db 181 VKQTHVPLFSLQCGAGFPLNQGSEVLASVGSMTIGIDHSLYTGSLSWYTPIRREYYE 240
QY 241 VIIVREINGQDLMDCKEYNYDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTKFPDG 300
Db 241 VIIVREINGQDLMDCKEYNYDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTKFPDG 300
QY 301 FWLGEOLVCWQAGTTPNNIFPVISLYMGVNTQSFRIITLPOQYLRPEVDVATSODDCY 360
Db 301 FWLGEOLVCWQAGTTPNNIFPVISLYMGVNTQSFRIITLPOQYLRPEVDVATSODDCY 360
QY 361 KFAISQSGTGVMGAVIMEGFYVFDRAKRIQFAVSAACHVDEFTAAVEGFTVLDM 420
Db 361 KFAISQSGTGVMGAVIMEGFYVFDRAKRIQFAVSAACHVDEFTAAVEGFTVLDM 420
QY 421 DCGNIPQTDEST 433
Db 421 DCGNIPQTDEST 433

```

RESULT 5

ABR61929 ID ABR61929 standard; protein; 456 AA.

AC ABR61929;

DT 12-SEP-2003 (first entry)

DE Human promemapsin 2-T1 protein.

KM Memapsin 1; nootropic; neuroprotective; memapsin 2; beta secretase;
KW beta-amyloid protein; Alzheimer's disease; promemapsin 2-T1; human.

OS Homo sapiens.

PN W02003039454-A2.

PD 15-MAY-2003.

PF 23-OCT-2002; 2002WO-US034324.

PR 23-OCT-2001; 2001US-0335952P.

PR 27-NOV-2001; 2001US-0333545P.

PR 14-JAN-2002; 2002US-0348646P.

PR 20-JUN-2002; 2002US-0390804P.

PR 19-JUL-2002; 2002US-0397557P.

PR 19-JUL-2002; 2002US-0397619P.

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA (UNIT) UNIV ILLINOIS FOUND.

PI Ghosh AK, Tang J, Bilcer G, Chang W, Hong L, Koelsch G, Loy J;

PI Turner RT;

XX MPI: 2003-541410/51.

XX N-PSDB; ACC84850.

XX New peptide compounds are memapsin beta secretase inhibitors used for

XX treating Alzheimer's disease.

XX Claim 96; Fig 11; 407pp; English.

XX The invention relates to peptide compounds of specified formula. The

CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative

CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a human promemapsin 2-T1 protein
XX
SQ Sequence 456 AA;

Query Match 99.1%; Score 2267; DB 6; Length 456;
Best Local Similarity 99.1%; Pred. No. 8.4e-214;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 TQHGIRLRLSGTGAAPGLGELINLETDDEEPEERGRSGFVEMDNLKSGSQGYVEMTV 60
Db 24 TQHGIRLRLSGTGAAPGLGELINLETDDEEPEERGRSGFVEMDNLKSGSQGYVEMTV 83
QY 61 GSPPTQTLNIIIVDTSSNFAVGAPFLHRYRQQLSTYRDLKKGYYVPTTQKMEGEL 120
Db 84 GSPPTQTLNIIIVDTSSNFAVGAPFLHRYRQQLSTYRDLKKGYYVPTTQKMEGEL 143
QY 121 GTDLVSIHFGPNVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPDSTL 180
Db 121 GTDLVSIHFGPNVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPDSTL 180
QY 144 GTDLVSIHFGPNVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPDSTL 203
Db 144 GTDLVSIHFGPNVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPDSTL 203
QY 181 VKQTHVPLFSLQCGAGFPLNQGSEVLASVGSMTIGIDHSLYTGSLSWYTPIRREYYE 240
Db 204 VKQTHVPLFSLQCGAGFPLNQGSEVLASVGSMTIGIDHSLYTGSLSWYTPIRREYYE 263
QY 241 VIIVREINGQDLMDCKEYNYDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTKFPDG 300
Db 264 VIIVREINGQDLMDCKEYNYDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTKFPDG 323
QY 301 FWLGEOLVCWQAGTTPNNIFPVISLYMGVNTQSFRIITLPOQYLRPEVDVATSODDCY 360
Db 324 FWLGEOLVCWQAGTTPNNIFPVISLYMGVNTQSFRIITLPOQYLRPEVDVATSODDCY 383
QY 361 KFAISQSGTGVMGAVIMEGFYVFDRAKRIQFAVSAACHVDEFTAAVEGFTVLDM 420
Db 384 KFAISQSGTGVMGAVIMEGFYVFDRAKRIQFAVSAACHVDEFTAAVEGFTVLDM 443
QY 421 DCGNIPQTDEST 433
Db 444 DCGNIPQTDEST 456

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RESULT 6

AAB61334 ID AAB61334 standard; protein; 488 AA.

AC AAB61334;

DT 02-APR-2001 (first entry)

DE Memapsin 2 protein.

KM Memapsin 2; catalytic; Alzheimer's.

OS Homo sapiens.

PN W0200100663-A2.

PD 04-JAN-2001.

PF 27-JUN-2000; 2000WO-US017661.

PR 28-JUN-1999; 99US-0141363P.

PR 30-NOV-1999; 99US-0168060P.

PR 25-JAN-2000; 2000US-0177836P.

PR 27-JAN-2000; 2000US-0178368P.

PR 08-JUN-2000; 2000US-0210292P.

PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.

PA Tang JUN, Lin X, Koelsch G;

XX

DR WPI; 2001-102885/11.
XX Purified recombinant catalytically active memapsin 2, used to screen
PT inhibitors of it, which are used to treat and prevent Alzheimer's
PT disease.
PS Claim 2; Page 73-75; 86pp; English.
XX The present invention relates to a purified recombinant catalytically
XX active memapsin 2. The invention may be used for isolating inhibitors
CC which are used to treat or prevent Alzheimer's disease. The invention may
CC also be used to screen for individuals more genetically prone to develop
CC Alzheimer's disease
XX
SQ Sequence 488 AA;
Query Match 99.1%; Score 2267; DB 4; Length 488;
Best Local Similarity 99.1%; Pred. No. 9.3e-214;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TQHGIRLPRLRSGLGAPLGLLEINLETDEBPBEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
DB 9 TQHGIRLPRLRSGLGAPLGLRLPRETDEBPBEPGRGSGFVEMVDNLRGSGGGYVEMTV 68
QY 61 GSPPTNLILVDTGSSNFAVGAAPPLHRYRQRLSSTYRDLRKGVYPTQKKEGEL 120
DB 69 GSPPTNLILVDTGSSNFAVGAAPPLHRYRQRLSSTYRDLRKGVYPTQKKEGEL 128
QY 121 GTDLVSIHPGPVNTVRANIAAITESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 180
DB 129 GTDLVSIHPGPVNTVRANIAAITESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 188
QY 181 VKQTHVPLNLFSLQLCGAPFLNQSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREMYE 240
DB 189 VKQTHVPLNLFSLQLCGAPFLNQSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREMYE 248
QY 241 VIIIRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRAASTEFPPG 300
DB 249 VIIIRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRAASTEFPPG 308
QY 301 FNLGEOLVCMQAGTTPMNIFPVISLYLMGEVNTQSFRTITLPOQYLRPVEDVATSODDCY 360
DB 309 FNLGEOLVCMQAGTTPMNIFPVISLYLMGEVNTQSFRTITLPOQYLRPVEDVATSODDCY 368
QY 361 KPAISQSSSTGTVMGAVIMGFYVFPDRARKRIGFAVSACHVDEFTAAVEGPFVTLDME 420
DB 369 KPAISQSSSTGTVMGAVIMGFYVFPDRARKRIGFAVSACHVDEFTAAVEGPFVTLDME 428
QY 421 DCGYNIPQTDST 433
DB 429 DCGYNIPQTDST 441
RESULT 7
ID AAB6572 standard; protein; 488 AA.
XX AAB6572;
XX
DY 12-APR-2001 (first entry)
XX Human memapsin 2.
XX Human; memapsin 2; nootropic; neuroprotective; amyloid precursor protein;
KM APP; memapsin 2 inhibitor; Alzheimer's disease.
XX Homo sapiens.
XX OS
XX PN WO20010665-A2.
XX PD 04-JAN-2001.
XX PF 27-JUN-2000; 2000WO-US017742.

XX 28-JUN-1999; 99US-0141363P.
PR 30-NOV-1999; 99US-0168060P.
PR 25-JAN-2000; 2000US-0177836P.
PR 27-JAN-2000; 2000US-0178368P.
PR 08-JUN-2000; 2000US-0210292P.
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA (UNIT) UNIV ILLINOIS FOUND.
XX
XX Tang JUN, Hong L, Ghosh AK;
DR WPI: 2001-137933/14.
DR N-PSDB; AAF31848.
XX Novel memapsin 2 inhibitors which bind to active site of memapsin 2
PT having 2 catalytic aspartic residues and substrate binding cleft, used to
PT treat Alzheimer's disease by blocking amyloid precursor protein cleavage.
XX Example 1; Page 72-74; 86pp; English.
XX The present sequence is given in a specification relating to an inhibitor
CC of catalytically active memapsin 2. The inhibitor binds to the memapsin 2
CC active site, which is defined by the presence of two catalytic aspartic
CC residues and a substrate binding cleft. The inhibitor is useful for the
CC treatment and diagnosis of Alzheimer's disease. It is useful in screens
CC for individuals with a genetic predisposition to Alzheimer's disease. The
CC inhibitor is useful as a reagent for specifically binding to memapsin 2
CC or memapsin 2 analogues and for aiding in memapsin 2 isolation,
CC purification and characterisation
XX
SQ Sequence 488 AA;
Query Match 99.1%; Score 2267; DB 4; Length 488;
Best Local Similarity 99.1%; Pred. No. 9.3e-214;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TQHGIRLPRLRSGLGAPLGLLEINLETDEBPBEPGRGSGFVEMVDNLRGSGGGYVEMTV 60
DB 9 TQHGIRLPRLRSGLGAPLGLRLPRETDEBPBEPGRGSGFVEMVDNLRGSGGGYVEMTV 68
QY 61 GSPPTNLILVDTGSSNFAVGAAPPLHRYRQRLSSTYRDLRKGVYPTQKKEGEL 120
DB 69 GSPPTNLILVDTGSSNFAVGAAPPLHRYRQRLSSTYRDLRKGVYPTQKKEGEL 128
QY 121 GTDLVSIHPGPVNTVRANIAAITESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 180
DB 129 GTDLVSIHPGPVNTVRANIAAITESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 188
QY 181 VKQTHVPLNLFSLQLCGAPFLNQSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREMYE 240
DB 189 VKQTHVPLNLFSLQLCGAPFLNQSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREMYE 248
QY 241 VIIIRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRAASTEFPPG 300
DB 249 VIIIRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRAASTEFPPG 308
QY 301 FNLGEOLVCMQAGTTPMNIFPVISLYLMGEVNTQSFRTITLPOQYLRPVEDVATSODDCY 360
DB 309 FNLGEOLVCMQAGTTPMNIFPVISLYLMGEVNTQSFRTITLPOQYLRPVEDVATSODDCY 368
QY 361 KPAISQSSSTGTVMGAVIMGFYVFPDRARKRIGFAVSACHVDEFTAAVEGPFVTLDME 420
DB 369 KPAISQSSSTGTVMGAVIMGFYVFPDRARKRIGFAVSACHVDEFTAAVEGPFVTLDME 428
QY 421 DCGYNIPQTDST 433
DB 429 DCGYNIPQTDST 441
RESULT 8
ID ABG78372 standard; protein; 488 AA.
XX ABG78372

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XX AC ABG78372;
XX DT 15-NOV-2002 (first entry)
XX DE Human promemapsin 2.
XX KW Human; enzyme; memapsin 2; aspartic protease; beta secretase;
XX KW degenerative disease; Alzheimer's disease; amyloid precursor protein;
XX KW APP; neuroprotective; nootropic; inhibitor;
XX KW substrate side-chain preference.
XX OS Homo sapiens.
XX PN WO200253594-A2.
XX PD 11-JUL-2002.
XX PF 28-DEC-2001; 2001WO-US050826.
XX PR 28-DEC-2000; 2000US-0258705P.
XX PR 14-MAR-2001; 2001US-0275756P.
XX PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PI (UNIT ) UNIV ILLINOIS FOUND.
XX PT Tang JUN, Koelach G, Ghosh AK;
XX DR WPI; 2002-619088/66.
XX PT New memapsin 2 activity inhibitor useful in treatment of e.g. Alzheimer's
XX PT disease.
XX PS Claim 7; Fig 7; 7app; English.
XX CC The invention relates to an inhibitor of catalytically active memapsin 2
XX CC (an aspartic protease which can cleave at beta secretase sites), which
XX CC binds to the active site of memapsin 2 defined by the presence of two
XX CC catalytic aspartic residues and substrate binding cleft. Also included is
XX CC a method of determination of the substrate side-chain preference in
XX CC memapsin 2 sub-sites comprising: (a) reacting a mixture of memapsin 2
XX CC substrates with memapsin 2, and determining the sub-site preference of
XX CC memapsin 2 by determining relative initial hydrolysis rates of the
XX CC mixture of memapsin 2 substrates; or (b) preparing a combinatorial
XX CC library of memapsin 2 inhibitors containing a base sequence taken from
XX CC OM99-2 (Glu-Val-Asn-Leu-Ala-Glu-phe), probing the library of
XX CC inhibitors with memapsin 2 which binds to several inhibitors to generate
XX CC several bound memapsin 2, and detecting the bound memapsin 2 with an
XX CC antibody raised to memapsin 2 and an alkaline phosphatase conjugated
XX CC secondary antibody. The inhibitors may be used in the manufacture of a
XX CC medicament for the treatment of Alzheimer's disease since memapsin 2 may
XX CC be involved in the cleavage of amyloid precursor protein (APP), and for
XX CC determining the substrate side-chain preference in memapsin 2 sub-sites.
XX CC The present sequence represents human memapsin 2 (either prepromemapsin 2
XX CC or mature memapsin)
XX SQ Sequence 488 AA;
XX
Query Match          99.1%; Score 2267; DB 5; Length 488;
Best Local Similarity 99.1%; Pred. No. 9.3e-214;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 TQHGRLPLRSGLGAPLGLTINLETPDEPEEPGRSGFVEMVNDLRKSGQGYVVENTV 60
DB 9 TQHGRLPLRSGLGAPLGLTINLETPDEPEEPGRSGFVEMVNDLRKSGQGYVVENTV 68
QY 61 GSPPTQNLNLYDVTGSSNFAVGAHPFLHRYRQRLSTVYDRLKGVVYPTTQKMGCEL 120
DB 69 GSPPTQNLNLYDVTGSSNFAVGAHPFLHRYRQRLSTVYDRLKGVVYPTTQKMGCEL 128
QY 121 GTDLVSIHGPVNTVYRANIAAITESDKFFINGSMWEGITGLAVYELARPDDSLPFPDSL 180
DB 129 GTDLVSIHGPVNTVYRANIAAITESDKFFINGSMWEGITGLAVYELARPDDSLPFPDSL 188

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QY 181 VKQTHVPLNLSQLCGAGPPLNQSEVLASVGSMTIGSIDSLYTGSLMTPRIRREWYE 240
DB 189 VKQTHVPLNLSQLCGAGPPLNQSEVLASVGSMTIGSIDSLYTGSLMTPRIRREWYE 248
QY 241 VLIIVVEINGODLRKDCCKEYNDKSIYDSGTTNLRPKQVEAAVKSIIKAASTEKEPDG 300
DB 249 VLIIVVEINGODLRKDCCKEYNDKSIYDSGTTNLRPKQVEAAVKSIIKAASTEKEPDG 308
QY 301 FPLGEQLVQWQAGTTPMNIFFVISLYLMGEVTNOSFRITLLPQOYLAPVEVVAISODDCY 360
DB 309 FPLGEQLVQWQAGTTPMNIFFVISLYLMGEVTNOSFRITLLPQOYLAPVEVVAISODDCY 368
QY 361 KFAISQSSGTVMGAVIMEGFYVVFDPARKRIGFAVACVHDFRTAAVEGPFVTLDME 420
DB 369 KFAISQSSGTVMGAVIMEGFYVVFDPARKRIGFAVACVHDFRTAAVEGPFVTLDME 428
QY 421 DCGYNIPTQDTEST 433
DB 429 DCGYNIPTQDTEST 441

```

RESULT 9

AAU99488

ID AAU99488 standard; protein; 488 AA.

AAU99488;

07-OCT-2002 (first entry)

Human memapsin 2.

Human; memapsin 2; beta secretase; aspartic protease; APP;
 beta-amyloid precursor protein; amyloid plaque; Alzheimer's disease;
 neuroprotective; nootropic; enzyme.

Homo sapiens.

US2002049303-A1.

25-APR-2002.

28-FEB-2001; 2001US-00796264.

28-JUN-1999; 99US-0141363P.

30-NOV-1999; 99US-0168060P.

25-JAN-2000; 2000US-0177836P.

27-JAN-2000; 2000US-0178368P.

27-JUN-2000; 2000US-00604608.

(TANG/) TANG J J N.

(LINK/) LIN X.

(KOEL/) KOELISCH G.

(HONG/) HONG L.

Tang JUN, Lin X, Koelach G, Hong L;

WPI; 2002-507280/54.

N-PSDB; ABX88641.

New recombinant catalytically active memapsin 2, useful to screen for

inhibitors of Alzheimer's disease.

Claim 2; Page 22-23; 4app; English.

The present invention relates to methods for the production of purified,
 recombinant catalytically active, memapsin 2 (beta secretase). Memapsin
 2, a member of the aspartic protease family, cleaves beta-amyloid
 precursor protein (APP) found in amyloid plaques. The recombinant
 memapsin 2 is useful for identifying inhibitors of memapsin 2 in the
 design of drugs for the treatment and/or prevention of Alzheimer's
 disease. The recombinant memapsin 2 can be used to immunise against

CC Alzheimer's disease. The present sequence represents human memapsin 2
XX
SQ Sequence 488 AA;

Query Match 99.1%; Score 2267; DB 5; Length 488;
Best Local Similarity 99.1%; Pred. No. 9, 3e-214;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TQHGIRLPRLRSGLGAPLGLINLETDEBEPGRGRGSEVENVNLRGSGGGYVEMTV 60
DB 9 TQHGIRLPRLRSGLGAPLGLRLPRETDEBEPGRGRGSEVENVNLRGSGGGYVEMTV 68
QY 61 GSPPTLNTLVDTGSSNFVGAAPHPFLHRYTORQUSSTRDLRKGVVPTQKKEGEL 120
DB 69 GSPPTLNTLVDTGSSNFVGAAPHPFLHRYTORQUSSTRDLRKGVVPTQKKEGEL 128
QY 121 GTDLVSIHPGPNVTVRANIAITTESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 180
DB 129 GTDLVSIHPGPNVTVRANIAITTESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 188
QY 181 VQGVHVPNLFSIQLCGAGPFLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 240
DB 189 VQGVHVPNLFSIQLCGAGPFLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 248
QY 241 VTIIVVEINGODLKDCKEYNTDKSIYDSGTTNLRPKVYFEAAVKSITAASTEKFPDG 300
DB 249 VTIIVVEINGODLKDCKEYNTDKSIYDSGTTNLRPKVYFEAAVKSITAASTEKFPDG 308
QY 301 FMLGEOLVCMQAGTTPMNI FPIVSLYLMGEVNTQSFRTITLPOQYLRPEVDVATSDDDCY 360
DB 309 FMLGEOLVCMQAGTTPMNI FPIVSLYLMGEVNTQSFRTITLPOQYLRPEVDVATSDDDCY 368
QY 361 KFAISQSSGTGTVGAVIMGEFVYVFDRAKRIIGFAVSACHVDEFTAAVEGPFVTLDM 420
DB 369 KFAISQSSGTGTVGAVIMGEFVYVFDRAKRIIGFAVSACHVDEFTAAVEGPFVTLDM 428
QY 421 DCGYNIPQTDST 433
DB 429 DCGYNIPQTDST 441

RESULT 10

ABG76101
ID ABG76101 standard; protein; 488 AA.

XX
AC ABG76101;

DT 01-MAY-2003 (first entry)

XX Human partial memapsin 2.

XX Human; memapsin 2; beta-secretase; beta-amyloid precursor protein;

KW beta-amyloid peptide; Alzheimer's disease; neurotrophic; neuroprotective;

XX enzyme.

OS Homo sapiens.

XX
PN US2002164760-A1.

XX
PD 07-NOV-2002.

XX
PF 28-FEB-2001; 2001US-00795903.

XX
PR 28-JUN-1999; 99US-0141363P.

XX
PR 30-NOV-1999; 99US-0168060P.

XX
PR 25-JAN-2000; 2000US-0177836P.

XX
PR 27-JAN-2000; 2000US-0178368P.

XX
PR 08-JUN-2000; 2000US-0210292P.

XX
PR 27-JUN-2000; 2000US-00604608.

XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.

XX
XX Lin X, Koelsch G, Tang JUN;

XX
DR MPI: 2003-255218/25.
DR N-PSDB; ABX11591.
XX
PT New purified recombinant catalytically active memapsin 2 (beta-
PT secretase), useful for designing and screening of specific inhibitors for
PT the diagnosis, prevention and/or treatment of Alzheimer's disease.
XX
PS Claim 2; Page 22-23; 44pp; English.
XX
XX The invention relates to a purified recombinant catalytically active
XX memapsin 2, a beta-secretase which produces the beta-amyloid peptide from
XX the beta amyloid precursor protein. Also included are producing the above
XX memapsin 2 (comprising refolding the recombinant memapsin 2 under
XX conditions which dissociate and then slowly refold the enzyme into a
XX catalytically active form), isolating inhibitors of cleavage by memapsin
XX 2 (comprising adding to one or more potential inhibitors the memapsin 2
XX and a substrate for memapsin 2 and screening for decreased cleavage of
XX the substrate by the inhibitors), designing or obtaining inhibitors of
XX the memapsin 2 (comprising modelling an inhibitor based on the
XX crystalisation coordinates of memapsin 2 or the parameters given in the
XX specification), a database comprising binding properties and chemical
XX structures of compounds designed or screened by the method above and
XX treating or preventing Alzheimer's disease (comprising administering to a
XX patient an inhibitor of memapsin 2 which binds to the active site of the
XX memapsin 2 defined by the presence of 2 catalytic aspartic residues and
XX substrate binding cleft or immunising an individual with the above
XX memapsin 2 to elicit an amount of antibodies to reduce the cleavage by
XX endogenous memapsin 2). The memapsin 2 is useful in designing and/or
XX screening of specific inhibitors for the diagnosis, prevention and/or
XX treatment of Alzheimer's disease. The present sequence represents
XX memapsin 2
XX
SQ Sequence 488 AA;

Query Match 99.1%; Score 2267; DB 6; Length 488;
Best Local Similarity 99.1%; Pred. No. 9, 3e-214;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TQHGIRLPRLRSGLGAPLGLINLETDEBEPGRGRGSEVENVNLRGSGGGYVEMTV 60
DB 9 TQHGIRLPRLRSGLGAPLGLRLPRETDEBEPGRGRGSEVENVNLRGSGGGYVEMTV 68
QY 61 GSPPTLNTLVDTGSSNFVGAAPHPFLHRYTORQUSSTRDLRKGVVPTQKKEGEL 120
DB 69 GSPPTLNTLVDTGSSNFVGAAPHPFLHRYTORQUSSTRDLRKGVVPTQKKEGEL 128
QY 121 GTDLVSIHPGPNVTVRANIAITTESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 180
DB 129 GTDLVSIHPGPNVTVRANIAITTESDKPFINSNMEGILGLAYAEIARPDSDLPEPFDL 188
QY 181 VQGVHVPNLFSIQLCGAGPFLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 240
DB 189 VQGVHVPNLFSIQLCGAGPFLNQSEVLASVGSMTIGIDHSLYTGSLWYTPIRREMYE 248
QY 241 VTIIVVEINGODLKDCKEYNTDKSIYDSGTTNLRPKVYFEAAVKSITAASTEKFPDG 300
DB 249 VTIIVVEINGODLKDCKEYNTDKSIYDSGTTNLRPKVYFEAAVKSITAASTEKFPDG 308
QY 301 FMLGEOLVCMQAGTTPMNI FPIVSLYLMGEVNTQSFRTITLPOQYLRPEVDVATSDDDCY 360
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QY 361 KFAISQSSGTGTVGAVIMGEFVYVFDRAKRIIGFAVSACHVDEFTAAVEGPFVTLDM 420
DB 369 KFAISQSSGTGTVGAVIMGEFVYVFDRAKRIIGFAVSACHVDEFTAAVEGPFVTLDM 428
QY 421 DCGYNIPQTDST 433
DB 429 DCGYNIPQTDST 441

RESULT 11

ADA74817
 ID ADA74817 standard; protein; 488 AA.
 AC ADA74817;
 DT 20-NOV-2003 (first entry)
 DE Human memapsin 2 protein.
 XX
 XX memapsin 2; beta-secretase; amyloid precursor protein; APP;
 KW aspartic proteinase 2; ASP2; neurotrophic; neuroprotective;
 KM Alzheimer's disease; human; enzyme.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FH 1..180
 FT Region /note= "N-terminal lobe"
 FT Region 181..385
 FT Region /note= "C-terminal lobe"
 FT Region 359..393
 FT Region /note= "C-terminal extension"
 FT Region 369..376
 FT Region /note= "Beta-sheet 1"
 FT Region 378..383
 FT Region /note= "Alpha-helix 1"
 XX
 PN US6545127-B1.
 XX
 PD 08-APR-2003.
 XX
 PF 27-JUN-2000; 2000US-00604608.
 XX
 PR 28-JUN-1999; 99US-0141363P.
 PR 30-NOV-1999; 99US-0168060P.
 PR 25-JAN-2000; 2000US-0177836P.
 PR 27-JUN-2000; 2000US-0178368P.
 PR 08-JUN-2000; 2000US-0210292P.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PI Tang JUN, Lin X, Koelsch G, Hong L;
 DR WPI, 2003-566587/53.
 DR N-PSDB; ADA74816.
 XX
 PT Novel memapsin 2 protein that cleaves a beta-secretase site of an amyloid
 PT precursor protein is useful in the design and screening of specific
 PT inhibitors for treating and preventing Alzheimer's disease.
 XX
 PS Disclosure; Col 39-42; 44pp; English.
 XX
 XX The invention relates to a novel method which comprises the production of
 CC purified, catalytically active, recombinant memapsin 2 (beta-secretase)
 CC protein where the memapsin protein is expressed in a bacterial cell and
 CC cleaves the beta-secretase site of an amyloid precursor protein (APP).
 CC Memapsin 2, also known as aspartic proteinase 2 (ASP2), belongs to the
 CC aspartic protease family and demonstrates neurotrophic and neuroprotective
 CC activities. The protein of the invention may be useful in the design and
 CC screening of specific inhibitors which are useful in treating and
 CC preventing Alzheimer's disease. The current sequence is that of the human
 CC memapsin 2 protein of the invention.
 XX
 SQ Sequence 488 AA;

Query Match 99.1%; Score 2267; DB 6; Length 488;
 Best Local Similarity 99.1%; Pred. No. 9.3e-214;
 Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TOHGIRLPRLRSGLGAGAPLGLEINLETDEPEPEGRSGFVEMVDNLKSGSGGYVEMTV 60
 DB 9 TOHGIRLPRLRSGLGAGAPLGRLPRETDEPEPEGRSGFVEMVDNLKSGSGGYVEMTV 68

QY 61 GSPPTLTILVDTGSSNFAVGAAPFLHRRYYQRQLSSTYRDLKGVVVPYTGKMEGEL 120
 DB 69 GSPPTLTILVDTGSSNFAVGAAPFLHRRYYQRQLSSTYRDLKGVVVPYTGKMEGEL 128
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 DB 129 GTDLVSIHPGPNVTVRANIAAITESDKFFINGSMMEGILGLAYEIRPDSLEPPFDSL 188
 QY 181 VKQTHVPMFLFSLQCGAGFPLNOSFVLASVGSNIIIGIDHSLYTGSLMYTPIRREWYE 240
 DB 189 VKQTHVPMFLFSLQCGAGFPLNOSFVLASVGSNIIIGIDHSLYTGSLMYTPIRREWYE 248
 QY 241 VTIIVVEINQDILKMDCKEYNYDKSIYDSGTTNRLPKYFBAAVKSIKAASSTEKPPDG 300
 DB 249 VTIIVVEINQDILKMDCKEYNYDKSIYDSGTTNRLPKYFBAAVKSIKAASSTEKPPDG 308
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 DB 309 FVLGEQLVCMQAGTTPNNIFPVISLYLMGEVTNOSPFTILPOOYLAPVEDVATSDDCY 368
 QY 361 KFAISQSSGTVMGAVIMEGFYVFDPRARRKIGFAVSACHVHDEFRTAAVEGPFVTLDME 420
 DB 369 KFAISQSSGTVMGAVIMEGFYVFDPRARRKIGFAVSACHVHDEFRTAAVEGPFVTLDME 428
 QY 421 DCGYNIPTQTEST 433
 DB 429 DCGYNIPTQTEST 441

RESULT 12
 AAY94767
 ID AAY94767 standard; protein; 501 AA.
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 AC AAY94767;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE Human beta-secretase amino acid sequence.
 XX
 KW Beta-secretase; enzyme; amyloid plaque; Alzheimer's disease; human;
 KW Down's syndrome; amyloid angiopathy; gene therapy; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..45
 FT /label= putative signal peptide
 FT Protein 46..501
 FT /label= Beta-secretase

WO200058479-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 23-MAR-2000; 2000MO-US007755.
 XX
 PR 26-MAR-1999; 99US-00277229.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Citron M, Vassar RJ, Bennett BD;
 DR WPI, 2000-594643/56.
 DR N-PSDB; AAA8278.
 XX
 PT Isolated beta-secretase nucleic acids and encoded polypeptides, useful
 PT for diagnosis and gene therapy of Alzheimer's disease.
 XX
 PS Claim 1; Fig 4; 145pp; English.

CC This invention relates to 3 nucleotide sequences encoding beta-secretase
 CC proteins. Beta-secretase is an enzyme involved in the production of one
 CC of the components of amyloid plaques involved in Alzheimer's disease. The

invention includes an expression vector comprising the nucleotide sequence, a host cell comprising the expression vector, and a process for producing the protein through culturing the transformed cells. Also included in the invention are a polypeptide derivative of the beta-secretase protein, a fusion protein comprising beta-secretase fused to a heterologous amino acid sequence, and a method for modulating the levels of beta-secretase polypeptide in a mammal comprising administering the polynucleotide sequence. Beta-secretase exhibits neuroprotective and neurotrophic activity. The beta-secretase nucleotide sequence may be used to map locations of the beta-secretase gene and related genes on chromosomes and as hybridization probes in diagnostic assays to test for the presence of beta-secretase DNA or RNA, such as in Alzheimer's disease, Down's syndrome, and amyloid angiopathy. The nucleotide sequence may also be used as anti-sense inhibitors of beta-secretase expression, in gene therapy of Alzheimer's disease, and for the identification of compounds that modulate beta-secretase activity. Antibodies to the beta-secretase protein may be used for in vitro and in vivo diagnostic purposes to detect the presence of beta-secretase polypeptide in a body fluid or cell sample. The present sequence represents the human beta-secretase protein

Sequence 501 AA;

Query Match 99.1%; Score 2267; DB 3; Length 501;
Best Local Similarity 99.1%; Pred. No. 9.7e-214; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 3;

1 TOHGIRLPKRSIGGAPLGLLEINLEETDEBEPGRGRSFVEMVDNLRGSGGGYVEMTV 60
22 TQHGIRLPKRSIGGAPLGLRLPRETDEBEPGRGRSFVEMVDNLRGSGGGYVEMTV 81
61 GSPPTQNLTLVDTGSSNFVGAAPHPFLHRYRQQLSSTRDLRKGVVYPYTGKKEGEL 120
82 GSPPTQNLTLVDTGSSNFVGAAPHPFLHRYRQQLSSTRDLRKGVVYPYTGKKEGEL 141
121 GTDLVSIPIGPNVTYVANIATIESDKPFINSNMGGIIGLAAEYAEIARPDLSLEPFDSL 180
142 GTDLVSIPIGPNVTYVANIATIESDKPFINSNMGGIIGLAAEYAEIARPDLSLEPFDSL 201
181 VKQTHVPNLFSIQLCGAGPFLNQSSEVLASVGSMTIGIDHSIYTSLSLWTPPIRRMYEY 240
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241 VIIVRVEINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTEXEPDG 300
262 VIIVRVEINGODLKMDCKEYNDKSIYDSGTNLRLPKVFEAAVYSIKAASTEXEPDG 321
301 FWLGEOLVCMQAGTTTPMNIIPVVISLYLMGEVTVNOSFRITILLPOQYLARPVEDVATSDDDCY 360
322 FWLGEOLVCMQAGTTTPMNIIPVVISLYLMGEVTVNOSFRITILLPOQYLARPVEDVATSDDDCY 381
361 KFAISOSSTGTWGAIVMEGFYVFPDRAKRIGFAVSACHVDEFTAAVEGPFVTLDM 420
382 KFAISOSSTGTWGAIVMEGFYVFPDRAKRIGFAVSACHVDEFTAAVEGPFVTLDM 441
421 DCGYNIPQTDDEST 433
442 DCGYNIPQTDDEST 454

RESULT 13
AAB07896
ID AAB07896 standard; protein; 501 AA.

XX AAB07896;

XX 14-NOV-2000 (first entry)

XX Amino acid sequence of a human beta-secretase enzyme.

XX Beta-secretase; beta-amyloid precursor protein; beta-amyloid peptide;
KM amyloid plaque component; Alzheimer's disease; amyloidogenic disease;
XX inhibitor.

OS Homo sapiens.

XX WO200047618-A2.

XX 17-AUG-2000.

XX 10-FEB-2000; 2000WO-US003819.

XX 10-FEB-1999; 99US-0119571P.

XX 15-JUN-1999; 99US-0139172P.

XX (ELAN-) ELAN PHARM INC.

XX Anderson JP, Basi G, Doane MT, Frigon N, John V, Power M,
PI Sima S, Tatsuno G, Tung J, Wang S, Mcconlogue L,

XX WPI; 2000-533011/48.

XX N-PSDB; AAM59550, AAM59551.

XX Purified beta-secretase protein used in assays to discover inhibitors
PT which can be used for the treatment of amyloidogenic diseases e.g.
PT Alzheimer's disease.

XX Claim 17; Fig 2A; 121p; English.

CC The specification describes a beta-secretase enzyme. The enzyme cleaves
CC beta-amyloid precursor protein to produce beta-amyloid peptide. This
CC enzyme is therefore implicated in the production of amyloid plaque
CC components which accumulate in the brains of individuals afflicted with
CC Alzheimer's disease. Inhibitors of beta-secretase are administered to a
CC mammalian subject e.g. with Alzheimer's disease or Alzheimer's disease-
CC like pathology to test if they maintain or improve cognitive ability or
CC reduce the plaque burden. The compounds are used for the treatment of
CC amyloidogenic diseases e.g. Alzheimer's disease. The present sequence
CC represents a human beta-secretase enzyme

XX Sequence 501 AA;

Query Match 99.1%; Score 2267; DB 3; Length 501;
Best Local Similarity 99.1%; Pred. No. 9.7e-214; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 3;

1 TOHGIRLPKRSIGGAPLGLLEINLEETDEBEPGRGRSFVEMVDNLRGSGGGYVEMTV 60
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61 GSPPTQNLTLVDTGSSNFVGAAPHPFLHRYRQQLSSTRDLRKGVVYPYTGKKEGEL 120
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301 FWLGEOLVCMQAGTTTPMNIIPVVISLYLMGEVTVNOSFRITILLPOQYLARPVEDVATSDDDCY 360
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361 KFAISOSSTGTWGAIVMEGFYVFPDRAKRIGFAVSACHVDEFTAAVEGPFVTLDM 420
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421 DCGYNIPQTDDEST 433
442 DCGYNIPQTDDEST 454

DR N-PSDB; ACC84849.

XX New peptide compounds are memapsin beta secretase inhibitors used for
PT treating Alzheimer's disease.
XX

PS Claim 98; Fig 9; 407pp; English.

XX The invention relates to peptide compounds of specified formula. The
CC compounds exhibit memapsin 2-beta secretase inhibitory activity relative
CC to memapsin 1-beta secretase and reduce the accumulation of beta-amyloid
CC protein. The compounds can be used for treating Alzheimer's disease. The
CC present sequence represents a human memapsin 2 protein (GenBank Index
CC (G1):6912266)
XX

SQ Sequence 501 AA;

Query Match 99.1%; Score 2267; DB 6; Length 501;

Best Local Similarity 99.1%; Pred. No. 9,7e-214; Mismatches 3; Indels 0; Gaps 0;

Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY	61	GSPPTLNI	LVDTGSSN	FAVGAAP	PHFLHRY	YQRLS	STYRDL	RKG	YVPTQ	KWEGEL
DB	82	GSPPTLNI	LVDTGSSN	FAVGAAP	PHFLHRY	YQRLS	STYRDL	RKG	YVPTQ	KWEGEL
QY	121	GTDLVSI	PHGPNVT	VRANIAA	TTESDK	PFINSN	WEGILG	LA	YAEIAR	PDDSL
DB	142	GTDLVSI	PHGPNVT	VRANIAA	TTESDK	PFINSN	WEGILG	LA	YAEIAR	PDDSL
QY	181	VKQTHV	PNLFSL	OLCGAG	FPPLNQ	SEVLAS	VGSMI	IGIDH	SLY	TGSLW
DB	202	VKQTHV	PNLFSL	OLCGAG	FPPLNQ	SEVLAS	VGSMI	IGIDH	SLY	TGSLW
QY	241	VIIIVR	VEINGD	LKMDCKE	KNYDKS	IVDSG	TNLR	LPKV	FEA	AVKSI
DB	262	VIIIVR	VEINGD	LKMDCKE	KNYDKS	IVDSG	TNLR	LPKV	FEA	AVKSI
QY	301	FMLGE	QLV	WQAG	TTPMNI	FPV	ISLY	LMGE	V	NQSF
DB	322	FMLGE	QLV	WQAG	TTPMNI	FPV	ISLY	LMGE	V	NQSF
QY	361	KFAIS	QSSTG	TWGA	VIMGE	GFYV	FPD	RKR	IGFA	VSACH
DB	382	KFAIS	QSSTG	TWGA	VIMGE	GFYV	FPD	RKR	IGFA	VSACH
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
497.278 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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1	2267	99.1	480	4	US-09-724-566A-66	Sequence 66, App1
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3	2267	99.1	488	4	US-09-604-308D-2	Sequence 2, App1
4	2267	99.1	501	4	US-09-548-372D-4	Sequence 4, App1
5	2267	99.1	501	4	US-09-548-367D-4	Sequence 4, App1
6	2267	99.1	501	4	US-09-551-853D-4	Sequence 4, App1
7	2267	99.1	501	4	US-09-724-566A-2	Sequence 2, App1
8	2267	99.1	501	4	US-09-416-901B-4	Sequence 4, App1
9	2267	99.1	501	4	US-09-548-376D-4	Sequence 4, App1
10	2267	99.1	501	4	US-09-799-927A-4	Sequence 4, App1
11	2267	99.1	501	4	US-09-548-373D-4	Sequence 4, App1
12	2267	99.1	501	4	US-09-795-847B-4	Sequence 4, App1
13	2267	99.1	501	4	US-09-548-366F-4	Sequence 4, App1
14	2267	99.1	501	4	US-09-940-016-6810	Sequence 610, App1
15	2267	99.1	501	4	US-09-548-368D-4	Sequence 4, App1
16	2267	99.1	501	4	US-09-794-925A-4	Sequence 4, App1
17	2267	99.1	501	4	US-09-471-669A-2	Sequence 2, App1
18	2267	99.1	501	4	US-09-806-194A-4	Sequence 4, App1
19	2267	99.1	503	4	US-09-604-608-3	Sequence 3, App1
20	2267	99.1	578	4	US-09-940-016-10253	Sequence 10253, App1
21	2267	99.1	453	4	US-09-548-372D-30	Sequence 30, App1
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23	2262	99.9	453	4	US-09-551-853D-30	Sequence 30, App1
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31	2262	98.9	453	4	US-09-548-366D-30	Sequence 30, Appl
32	2262	98.9	453	4	US-09-794-925A-30	Sequence 30, Appl
33	2262	98.9	453	4	US-09-805-194A-30	Sequence 30, Appl
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35	2262	98.9	459	4	US-09-548-367D-32	Sequence 32, Appl
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37	2262	98.9	459	4	US-09-416-901B-32	Sequence 32, Appl
38	2262	98.9	459	4	US-09-548-376D-32	Sequence 32, Appl
39	2262	98.9	459	4	US-09-794-927A-32	Sequence 32, Appl
40	2262	98.9	459	4	US-09-548-373D-32	Sequence 32, Appl
41	2262	98.9	459	4	US-09-795-847B-32	Sequence 32, Appl
42	2262	98.9	459	4	US-09-865-414-32	Sequence 32, Appl
43	2262	98.9	459	4	US-09-548-366F-32	Sequence 32, Appl
44	2262	98.9	459	4	US-09-548-366D-32	Sequence 32, Appl
45	2262	98.9	459	4	US-09-794-925A-32	Sequence 32, Appl

ALIGNMENTS

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RESULT 1
; US-09-724-566A-66
; Sequence 66, Application US/0974566A
; Patent No. 6627739
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurqibal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6627739mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEWC2
; CURRENT APPLICATION NUMBER: US/09/724,566A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 66
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-566A-66

Query Match      99.1%; Score 2267; DB 4; Length 480;
Beet Local Similarity 99.1%; Pred. No. 1.2e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0

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DB 1 TQHGRIPLRSGLGAPLGLRIINLTDEBPBPGRGSFVENVDLRKGSGGYVEMTV 60

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DB 61 GSPPTNIIIVDTGSSNFVAGAAPPLHARRYQROLSSTYRDLKRGVYPTQGMKEGL 120

QY 121 GTDLVSIHGGNMYRRANIIAITSDEKPFINGSNMEGLGLAAYRIARPPDLSLPPFDST 180
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DB 121 GTDLVSIHGGNMYRRANIIAITSDEKPFINGSNMEGLGLAAYRIARPPDLSLPPFDST 180

QY 121 GTDLVSIHGGNMYRRANIIAITSDEKPFINGSNMEGLGLAAYRIARPPDLSLPPFDST 180
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DB 121 GTDLVSIHGGNMYRRANIIAITSDEKPFINGSNMEGLGLAAYRIARPPDLSLPPFDST 180

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QY 241 VIVRVEINGDGLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTEKEPPDG 300
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; Sequence 66, Application US/09471669A
; Patent No. 6830918
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Bassi, Guribhai
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, No. 6830918mand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; APPLICANT: Elan Pharmaceuticals, Inc.
; TITLE OF INVENTION: BETA-SECRETASE ENZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 015270-006430US
; CURRENT APPLICATION NUMBER: US/09/471,669A
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: US 60/114,408
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-669A-66
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Query Match 99.1%; Score 2267; DB 4; Length 480;
Best Local Similarity 99.1%; Pred. No. 1.2e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 TQHGIRLPRLSGGLGAPLGLEINLETTDEEPEEPPRRSGFVEMVDNLKSGSGGGYVEMTV 60
DB 1 TQHGIRLPRLSGGLGAPLGLEINLETTDEEPEEPPRRSGFVEMVDNLKSGSGGGYVEMTV 60
QY 61 GSPPTQNLIVDTSSNPAVGAHPFLHRYRQQLSSTRDLRKGYVVPYTGKMEGEL 120
DB 61 GSPPTQNLIVDTSSNPAVGAHPFLHRYRQQLSSTRDLRKGYVVPYTGKMEGEL 120
QY 121 GTDLVSIIPHGBNVTVRANIAITESDKFINGSNWEGIIGLAVAEIARPDSDLEPPFDL 180
DB 121 GTDLVSIIPHGBNVTVRANIAITESDKFINGSNWEGIIGLAVAEIARPDSDLEPPFDL 180
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QY 181 VKQTHVNLFSLOLCGAGFPLNOSSEVLASVGSMTICGIDHSIYTGSLMTTPIRREMYE 240
DB 181 VKQTHVNLFSLOLCGAGFPLNOSSEVLASVGSMTICGIDHSIYTGSLMTTPIRREMYE 240
QY 241 VIVRVEINGDGLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTEKEPPDG 300
DB 241 VIVRVEINGDGLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIIKAASSTEKEPPDG 300
QY 301 FVLGEOLVCMQAGTTPMNIFFVVISLYLMGEVTNOSFRITLLPOQYLRPVEDVATSODDCY 360
DB 301 FVLGEOLVCMQAGTTPMNIFFVVISLYLMGEVTNOSFRITLLPOQYLRPVEDVATSODDCY 360
QY 361 KFAISOSSTGTVMGAVIMEGFYVFDPRARRIGFAVSACHVHDEFRTAAVEGPFVTLDM 420
DB 361 KFAISOSSTGTVMGAVIMEGFYVFDPRARRIGFAVSACHVHDEFRTAAVEGPFVTLDM 420
QY 421 DCGYNIPQTDSEST 433
DB 421 DCGYNIPQTDSEST 433
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RESULT 3
US-09-604-608-2
; Sequence 2, Application US/09604608
; Patent No. 6545127
; GENERAL INFORMATION:
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Lin, Xinli
; APPLICANT: Koelsch, Gerald
; TITLE OF INVENTION: Catalytically Active Recombinant Memapsin and Methods
; FILE REFERENCE: OMR 179
; CURRENT APPLICATION NUMBER: US/09/604,608
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/141,363
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: 60/168,060
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: 60/177,836
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 60/178,368
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: 60/210,292
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Purified Memapsin 2
; OTHER INFORMATION: Amino Acids 28-48 are remnant putative propeptide
; OTHER INFORMATION: residues
; OTHER INFORMATION: Amino Acids 58-61, 78, 80, 82-83, 116, 118-121,
; OTHER INFORMATION: 156, 166, 174, 246, 274, 276, 278-281, 283, and
; OTHER INFORMATION: 376-377 are residues in contact with the OM99-2
; OTHER INFORMATION: inhibitor
; OTHER INFORMATION: Amino acids 54-57, 61-68, 73-80, 86-89, 109-111,
; OTHER INFORMATION: 113-118, 123-134, 143-154, 165-168, 198-202, and
; OTHER INFORMATION: 220-224 are N-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 184-191 and 210-217 are N-lobe Helices
; OTHER INFORMATION: Amino acids 237-240, 247-249, 251-256, 259-260,
; OTHER INFORMATION: 273-275, 282-285, 316-318, 331-336, 342-348,
; OTHER INFORMATION: 354-357, 366-370, 372-375, 380-383, 390-395,
; OTHER INFORMATION: 400-405, and 418-420 are C-lobe Beta Strands
; OTHER INFORMATION: Amino Acids 286-299, 307-310, 350-353, 384-387,
; OTHER INFORMATION: and 427-431 are C-lobe Helices
US-09-604-608-2
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Query Match 99.1%; Score 2267; DB 4; Length 488;
Best Local Similarity 99.1%; Pred. No. 1.2e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY      1  TQHGIRLPKRSGLGCAPLGLIETLETDEBEERGRGSPFEMTDNLRGKGGQGYVEMTV  60
Db      9  TQHGIRLPKRSGLGCAPLGLIRPRETDBEERGRGSPFEMTDNLRGKGGQGYVEMTV  68
QY      61  GSPPTLNLVTGSSNFAVGAAPHFPLHRYRQOLSTYRDLRKGYVPEYTOGMEGEL  120
Db      69  GSPPTLNLVTGSSNFAVGAAPHFPLHRYRQOLSTYRDLRKGYVPEYTOGMEGEL  128
QY      121  GTDLVSIHPGNVTVRANIAAITESDKFFINGSNWEIIGLAVAEIARPDLSLEPFDSL  180
Db      129  GTDLVSIHPGNVTVRANIAAITESDKFFINGSNWEIIGLAVAEIARPDLSLEPFDSL  188
QY      161  VKQTHVPMFLSIQLCAGAPPLNOSVTLASVGSMMIIGDISHLYTGSJLWTPPIREMYE  240
Db      189  VKQTHVPMFLSIQLCAGAPPLNOSVTLASVGSMMIIGDISHLYTGSJLWTPPIREMYE  248
QY      241  VTIIVVEINIGDOLXMDCKEKNYKSIYDSGTTNLRPKVFEAAVKSIIKAASSTKEPPDG  300
Db      249  VTIIVVEINIGDOLXMDCKEKNYKSIYDSGTTNLRPKVFEAAVKSIIKAASSTKEPPDG  308
QY      301  FWLGEOLVCMQAGTTPMNIFPVISLYLMGEVTVNSFRITLLPQOYLRPVEDVATSODDCY  360
Db      309  FWLGEOLVCMQAGTTPMNIFPVISLYLMGEVTVNSFRITLLPQOYLRPVEDVATSODDCY  368
QY      361  KFAISQSSGTGYMGAIVIMEGFYVFPDRAKRIIGFVAGSACHVHDEPRTAAVEGPTVTLDM  420
Db      369  KFAISQSSGTGYMGAIVIMEGFYVFPDRAKRIIGFVAGSACHVHDEPRTAAVEGPTVTLDM  428
QY      421  DCGYNIPQTDDEST  433
Db      429  DCGYNIPQTDDEST  441

RESULT 4
US-09-548-372D-4
/ Sequence 4, Application US/09548372D
/ Patent No. 6420534
/ GENERAL INFORMATION:
/ APPLICANT: GURNEY ET AL.
/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
/ FILE REFERENCE: 29915/62801
/ CURRENT APPLICATION NUMBER: US/09/548, 372D
/ CURRENT FILING DATE: 2000-04-12
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-548-372D-4

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Query Match	Best Local Similarity	Score	DB 4	Length	501
Matches	429	Conservative	1	Mismatches	3
				Indels	0
				Gaps	0
Qy	1	TOHGIRLPKSGTGCAFLGELINLEDEEPPERRGSGVEVNDNLKSGSGGYVEMTV	60		
Db	22	TOHGIRLPKSGTGCAFLGELINLEDEEPPERRGSGVEVNDNLKSGSGGYVEMTV	81		
Qy	61	GSPPTQLNLIVDTGSSNFAVGAAHPHFLIRYROROLSTFYRDLKGVYPTTGKMEGL	120		
Db	82	GSPPTQLNLIVDTGSSNFAVGAAHPHFLIRYROROLSTFYRDLKGVYPTTGKMEGL	141		

QY	121	GTDLVSIHGHWYVYRANIAAITEDEKFFINSNMEGILGLAVARAPDSDLEPEPDSL	180
Db	142	GTDLVSIHGHWYVYRANIAAITEDEKFFINSNMEGILGLAVARAPDSDLEPEPDSL	201
QY	181	VKQTHVPLFSLIOLCGAGPPLNOSVLSVGSMTIIGIDHSLYTGSWYTPIRREMYE	240
Db	202	VKQTHVPLFSLIOLCGAGPPLNOSVLSVGSMTIIGIDHSLYTGSWYTPIRREMYE	261
QY	241	VIIYVEINGODLKMDCKEYNYDKSI VDSGTNNLRPKKVFEAAVYSIKAASTEKFPDG	300
Db	262	VIIYVEINGODLKMDCKEYNYDKSI VDSGTNNLRPKKVFEAAVYSIKAASTEKFPDG	321
QY	301	FMLGSOLVCWQAGTTPPANI PVIYSIYLNGEVTNOSFRITILPQOYRARPEDVATSODDC	360
Db	322	FMLGSOLVCWQAGTTPPANI PVIYSIYLNGEVTNOSFRITILPQOYRARPEDVATSODDC	381
QY	361	KFAISQSTGYTMGAVIMEGFVYVDPDAPARKIGFAPSACHVDEPFTAAVEGPFVTLME	420
Db	382	KFAISQSTGYTMGAVIMEGFVYVDPDAPARKIGFAPSACHVDEPFTAAVEGPFVTLME	441
QY	421	DCGVNIPOTDEST	433
Db	442	DCGVNIPOTDEST	454

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RESULT 5
US-09-548-367D-4
; Sequence 4, Application US/09548367D
; Patent No. 6440698
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,367D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: FRT
; ORGANISM: Homo sapiens
US-09-548-367D-4

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Query Match	Similarity	99.1%	Score 2267;	DB 4	Length 501;
Best Local	Similarity	99.1%	Pred. No. 1.3e-235;		
Matches	Conservative	1;	Mismatches	3;	Indels 0; Gaps 0
Qy	1	TOHGIRLPLRSLGAGAPLGLINLTDEPEEPGRGSEVEMVDNLRGKSGGCVYEMTV	60		
Db	22	TQHGIRLPLRSLGAGAPLGLIRLPRPTDEPEEPGRGSEVEMVDNLRGKSGGCVYEMTV	81		
Qy	61	GSPPTNTLVYTGSSNFVAGAAPPLPHRYXQROLSSYRDLRGKVYVPTQGMKEGL	120		
Db	82	GSPPTNTLVYTGSSNFVAGAAPPLPHRYXQROLSSYRDLRGKVYVPTQGMKEGL	141		
Qy	121	GTDLVSIPIHPGVVYRANITAIITSDKCFINSNNEGIIGLAVASIAIAPDDSLSEFPDLSL	180		
Db	142	GTDLVSIPIHPGVVYRANITAIITSDKCFINSNNEGIIGLAVASIAIAPDDSLSEFPDLSL	201		
Qy	181	VQOTHPNLFSLQLGAGPELNQSSVLA SVGSSMTIGGIDHSLYGSIMYTPIRREMYE	240		
Db	202	VQOTHPNLFSLQLGAGPELNQSSVLA SVGSSMTIGGIDHSLYGSIMYTPIRREMYE	261		
Qy	241	VLIIVREINGODLRKDCKEYNYSKSI VDSGTNNLRPKKVFEEAAYSKIAASSTEFPPDG	300		

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Db      262 VIIVREINIGDGLKMDCKEYNDKSI VDSGTTNLRPKVFEAAVKSIKAASTKFPDG 321
QY      301 FWLGEQLVCMQAGTTPMNIFFVYISLYLMGEVYNOSFRITTLPOQYLRAVEDVATSODDCY 360
Db      322 FWLGEQLVCMQAGTTPMNIFFVYISLYLMGEVYNOSFRITTLPOQYLRAVEDVATSODDCY 381
QY      361 KFAISQSSGTGMGAVIMEGFYVVDRAKRIIGFAVSACHVHDEFRTAAVEGPFVTL DME 420
Db      382 KFAISQSSGTGMGAVIMEGFYVVDRAKRIIGFAVSACHVHDEFRTAAVEGPFVTL DME 441
QY      421 DCGYNIPOTDEST 433
Db      442 DCGYNIPOTDEST 454

RESULT 6
US-09-551-853D-4
/ Sequence 4, Application US/09551853D
/ Patent No. 6500667
/ GENERAL INFORMATION:
/ APPLICANT: GURNEY ET AL.
/ TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
/ FILE REFERENCE: 29915/6280L
/ CURRENT APPLICATION NUMBER: US/09/551,853D
/ PRIOR FILING DATE: 2000-04-18
/ PRIOR APPLICATION NUMBER: US 60/155,493
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 09/404,133
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: PCT/US99/20881
/ PRIOR FILING DATE: 1999-09-23
/ PRIOR APPLICATION NUMBER: US 60/101,594
/ PRIOR FILING DATE: 1998-09-24
/ NUMBER OF SEQ ID NOS: 73
/ SOFTWARE: PatentIn version 3.1
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-551-853D-4

Query Match      99.1%; Score 2267; DB 4; Length 501;
Best Local Similarity 99.1%; Pred. No. 1.3e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TQHGIRLPRLRSGLGAPLGLIETNLETDDEPEERGRGSEFVEMVDNLRGSGGGYVEMTV 60
Db      22 TQHGIRLPRLRSGLGAPLGLIETNLETDDEPEERGRGSEFVEMVDNLRGSGGGYVEMTV 81
QY      61 GSPPTNLINLVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVYVPTQGWEGEL 120
Db      82 GSPPTNLINLVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVYVPTQGWEGEL 141
QY      121 GTDLVSIPIHGPVNTVRANIAAITESDKPFINSNNEGILGLAYAEIARPDLSLEFPDSL 180
Db      142 GTDLVSIPIHGPVNTVRANIAAITESDKPFINSNNEGILGLAYAEIARPDLSLEFPDSL 201
QY      181 VKQTHVPNLFSIQLGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSIMYPIRREWEYE 240
Db      202 VKQTHVPNLFSIQLGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSIMYPIRREWEYE 261
QY      241 VIIVREINIGDGLKMDCKEYNDKSI VDSGTTNLRPKVFEAAVKSIKAASTKFPDG 300
Db      262 VIIVREINIGDGLKMDCKEYNDKSI VDSGTTNLRPKVFEAAVKSIKAASTKFPDG 321
QY      301 FWLGEQLVCMQAGTTPMNIFFVYISLYLMGEVYNOSFRITTLPOQYLRAVEDVATSODDCY 360
Db      322 FWLGEQLVCMQAGTTPMNIFFVYISLYLMGEVYNOSFRITTLPOQYLRAVEDVATSODDCY 381
QY      361 KFAISQSSGTGMGAVIMEGFYVVDRAKRIIGFAVSACHVHDEFRTAAVEGPFVTL DME 420
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Db      382 KFAISQSSGTGMGAVIMEGFYVVDRAKRIIGFAVSACHVHDEFRTAAVEGPFVTL DME 441
QY      421 DCGYNIPOTDEST 433
Db      442 DCGYNIPOTDEST 454

RESULT 7
US-09-724-566A-2
/ Sequence 2, Application US/09724566A
/ Patent No. 6627739
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Basl, Gurigbal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Erligon, No. 6627739mand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatsuno, Gwen
/ APPLICANT: Tung, Jay
/ APPLICANT: Wang, Shuwen
/ APPLICANT: McConlogue, Lisa
/ TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
/ FILE REFERENCE: 228-US-NEWC2
/ CURRENT APPLICATION NUMBER: US/09/724,566A
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: US 09/501,708
/ PRIOR FILING DATE: 2000-02-10
/ PRIOR APPLICATION NUMBER: 60/119,571
/ PRIOR FILING DATE: 1999-02-10
/ PRIOR APPLICATION NUMBER: 60/139,172
/ PRIOR FILING DATE: 1999-06-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 501
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-724-566A-2

Query Match      99.1%; Score 2267; DB 4; Length 501;
Best Local Similarity 99.1%; Pred. No. 1.3e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 TQHGIRLPRLRSGLGAPLGLIETNLETDDEPEERGRGSEFVEMVDNLRGSGGGYVEMTV 60
Db      22 TQHGIRLPRLRSGLGAPLGLIETNLETDDEPEERGRGSEFVEMVDNLRGSGGGYVEMTV 81
QY      61 GSPPTNLINLVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVYVPTQGWEGEL 120
Db      82 GSPPTNLINLVDTGSSNFVGAAPHPFLHRYRQRLSSTYRDLRGVYVPTQGWEGEL 141
QY      121 GTDLVSIPIHGPVNTVRANIAAITESDKPFINSNNEGILGLAYAEIARPDLSLEFPDSL 180
Db      142 GTDLVSIPIHGPVNTVRANIAAITESDKPFINSNNEGILGLAYAEIARPDLSLEFPDSL 201
QY      181 VKQTHVPNLFSIQLGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSIMYPIRREWEYE 240
Db      202 VKQTHVPNLFSIQLGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSIMYPIRREWEYE 261
QY      241 VIIVREINIGDGLKMDCKEYNDKSI VDSGTTNLRPKVFEAAVKSIKAASTKFPDG 300
Db      262 VIIVREINIGDGLKMDCKEYNDKSI VDSGTTNLRPKVFEAAVKSIKAASTKFPDG 321
QY      301 FWLGEQLVCMQAGTTPMNIFFVYISLYLMGEVYNOSFRITTLPOQYLRAVEDVATSODDCY 360
Db      322 FWLGEQLVCMQAGTTPMNIFFVYISLYLMGEVYNOSFRITTLPOQYLRAVEDVATSODDCY 381
QY      361 KFAISQSSGTGMGAVIMEGFYVVDRAKRIIGFAVSACHVHDEFRTAAVEGPFVTL DME 420
Db      382 KFAISQSSGTGMGAVIMEGFYVVDRAKRIIGFAVSACHVHDEFRTAAVEGPFVTL DME 441
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QY 421 DCGYNIPQTDST 433
Db 442 DCGYNIPQTDST 454

RESULT 8

US-09-416-901B-4
; Sequence 4, Application US/09416901B
; Patent No. 6699671
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES THEREOF
; FILE REFERENCE: 29915/6280A
; CURRENT APPLICATION NUMBER: US/09/416,901B
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-416-901B-4

Query Match 99.1%; Score 2267; DB 4; Length 501;

Best Local Similarity 99.1%; Pred. No. 1,3e-235; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 3;

QY 1 TONGIRLPLRSGAGAPLGLIEINLETDEEPEERGRGSFVEMVDNLRGSGGGYVEMTV 60
Db 22 TONGIRLPLRSGAGAPLGLRLPRETDEEPEERGRGSFVEMVDNLRGSGGGYVEMTV 81
QY 61 GSPPTNLILVDTGSSNFAVGAAHPFLHRYRQRLSSTRDLRKGVYVPTQKMEGL 120
Db 82 GSPPTNLILVDTGSSNFAVGAAHPFLHRYRQRLSSTRDLRKGVYVPTQKMEGL 141
QY 121 GTDLVSIPIPGPNVTYRANIAAITESDKPFINGSNMEGILGLAYAEIARPDLSLEPFDSL 180
Db 142 GTDLVSIPIPGPNVTYRANIAAITESDKPFINGSNMEGILGLAYAEIARPDLSLEPFDSL 201
QY 181 VKQTHVNLFSIQLCGAGPFLNQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREMYE 240
Db 202 VKQTHVNLFSIQLCGAGPFLNQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREMYE 261
QY 241 VIIIVAEINGODLRKDCKEYNYSIVDSGTTNLRPKKVFPAAVSIRKASSTKXEPDG 300
Db 262 VIIIVAEINGODLRKDCKEYNYSIVDSGTTNLRPKKVFPAAVSIRKASSTKXEPDG 321
QY 301 FWLGEOLVCMQAGTTPMNIIPVVISLYLMGEVYNOSFRITILPOOYLARPEVDVATSDDCY 360
Db 322 FWLGEOLVCMQAGTTPMNIIPVVISLYLMGEVYNOSFRITILPOOYLARPEVDVATSDDCY 381
QY 361 KFAISQSSGTWAGAVIMEGFYVFPDARKRIGFAVSAHVHDEFRTAAVEGPFVTLDM 420
Db 382 KFAISQSSGTWAGAVIMEGFYVFPDARKRIGFAVSAHVHDEFRTAAVEGPFVTLDM 441
QY 421 DCGYNIPQTDST 433
Db 442 DCGYNIPQTDST 454

RESULT 9
US-09-548-376D-4
; Sequence 4, Application US/09548376D

; Patent No. 6706485

; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 29915/6280F
; CURRENT APPLICATION NUMBER: US/09/548,376D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-376D-4

Query Match 99.1%; Score 2267; DB 4; Length 501;

Best Local Similarity 99.1%; Pred. No. 1,3e-235; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 3;

QY 1 TONGIRLPLRSGAGAPLGLIEINLETDEEPEERGRGSFVEMVDNLRGSGGGYVEMTV 60
Db 22 TONGIRLPLRSGAGAPLGLRLPRETDEEPEERGRGSFVEMVDNLRGSGGGYVEMTV 81
QY 61 GSPPTNLILVDTGSSNFAVGAAHPFLHRYRQRLSSTRDLRKGVYVPTQKMEGL 120
Db 82 GSPPTNLILVDTGSSNFAVGAAHPFLHRYRQRLSSTRDLRKGVYVPTQKMEGL 141
QY 121 GTDLVSIPIPGPNVTYRANIAAITESDKPFINGSNMEGILGLAYAEIARPDLSLEPFDSL 180
Db 142 GTDLVSIPIPGPNVTYRANIAAITESDKPFINGSNMEGILGLAYAEIARPDLSLEPFDSL 201
QY 181 VKQTHVNLFSIQLCGAGPFLNQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREMYE 240
Db 202 VKQTHVNLFSIQLCGAGPFLNQSEVLASVSGSMIIGIDHSLYTGSLWYTPIRREMYE 261
QY 241 VIIIVAEINGODLRKDCKEYNYSIVDSGTTNLRPKKVFPAAVSIRKASSTKXEPDG 300
Db 262 VIIIVAEINGODLRKDCKEYNYSIVDSGTTNLRPKKVFPAAVSIRKASSTKXEPDG 321
QY 301 FWLGEOLVCMQAGTTPMNIIPVVISLYLMGEVYNOSFRITILPOOYLARPEVDVATSDDCY 360
Db 322 FWLGEOLVCMQAGTTPMNIIPVVISLYLMGEVYNOSFRITILPOOYLARPEVDVATSDDCY 381
QY 361 KFAISQSSGTWAGAVIMEGFYVFPDARKRIGFAVSAHVHDEFRTAAVEGPFVTLDM 420
Db 382 KFAISQSSGTWAGAVIMEGFYVFPDARKRIGFAVSAHVHDEFRTAAVEGPFVTLDM 441
QY 421 DCGYNIPQTDST 433
Db 442 DCGYNIPQTDST 454

RESULT 10

US-09-794-927A-4
; Sequence 4, Application US/09794927A

; Patent No. 6727074
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280FG
; CURRENT APPLICATION NUMBER: US/09/794,927A
; CURRENT FILING DATE: 2001-02-27

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; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-927A-4

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Query Match          99.1%; Score 2267; DB 4; Length 501;
Best Local Similarity 99.1%; Pred. No. 1.3e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TONGIRLPLRSGLGAPLGLINLETDEEPEEPGRGSPFVEMVDNLKSGGQGYVEMTV 60
DB 22 TONGIRLPLRSGLGAPLGLRLPRETDEEPEEPGRGSPFVEMVDNLKSGGQGYVEMTV 81
QY 61 GSPPTNTLIIVDTSSNFAVGAAPHPLHRYORQLSSTRDLRKGVYVPTQKMEGEL 120
DB 82 GSPPTNTLIIVDTSSNFAVGAAPHPLHRYORQLSSTRDLRKGVYVPTQKMEGEL 141
QY 121 GTDLVSIIPHGNVTVRANIAITSDKFFINGSNMEGILGLAYAEIARPDLSLEPFDSL 180
DB 142 GTDLVSIIPHGNVTVRANIAITSDKFFINGSNMEGILGLAYAEIARPDLSLEPFDSL 201
QY 181 VKOTHPNPLPSLQCGAFPLNOSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREWYE 240
DB 202 VKOTHPNPLPSLQCGAFPLNOSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREWYE 261
QY 241 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRKASTTEKFPDG 300
DB 262 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRKASTTEKFPDG 321
QY 301 FWLGEOLVCMQAGTTPMNIIPVLSIYLMEVTVNQSFRTITLPOQYLRPVEDVATSQDDCY 360
DB 322 FWLGEOLVCMQAGTTPMNIIPVLSIYLMEVTVNQSFRTITLPOQYLRPVEDVATSQDDCY 381
QY 361 KEAISQSTGTVMGAVIMEGFYVFPDARKRIGFAVSACHVDEFTAAVEGPFYTLME 420
DB 382 KEAISQSTGTVMGAVIMEGFYVFPDARKRIGFAVSACHVDEFTAAVEGPFYTLME 441
QY 421 DCGYNIPQTDDEST 433
DB 442 DCGYNIPQTDDEST 454

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RESULT 11
US-09-548-373D-4
; Sequence 4, Application US/09548373D
; Patent No. 6737510
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/62808
; CURRENT APPLICATION NUMBER: US/09/548,373D
; CURRENT FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24

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; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-373D-4

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Query Match          99.1%; Score 2267; DB 4; Length 501;
Best Local Similarity 99.1%; Pred. No. 1.3e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 TONGIRLPLRSGLGAPLGLINLETDEEPEEPGRGSPFVEMVDNLKSGGQGYVEMTV 60
DB 22 TONGIRLPLRSGLGAPLGLRLPRETDEEPEEPGRGSPFVEMVDNLKSGGQGYVEMTV 81
QY 61 GSPPTNTLIIVDTSSNFAVGAAPHPLHRYORQLSSTRDLRKGVYVPTQKMEGEL 120
DB 82 GSPPTNTLIIVDTSSNFAVGAAPHPLHRYORQLSSTRDLRKGVYVPTQKMEGEL 141
QY 121 GTDLVSIIPHGNVTVRANIAITSDKFFINGSNMEGILGLAYAEIARPDLSLEPFDSL 180
DB 142 GTDLVSIIPHGNVTVRANIAITSDKFFINGSNMEGILGLAYAEIARPDLSLEPFDSL 201
QY 181 VKOTHPNPLPSLQCGAFPLNOSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREWYE 240
DB 202 VKOTHPNPLPSLQCGAFPLNOSSEVLASVGSMTIIGIDHSLYTGSLWYTPIRREWYE 261
QY 241 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRKASTTEKFPDG 300
DB 262 VIIVRVEINGQDLKMDCKEYNDKSIYDSGTTNLRPKVFEAAVKSIRKASTTEKFPDG 321
QY 301 FWLGEOLVCMQAGTTPMNIIPVLSIYLMEVTVNQSFRTITLPOQYLRPVEDVATSQDDCY 360
DB 322 FWLGEOLVCMQAGTTPMNIIPVLSIYLMEVTVNQSFRTITLPOQYLRPVEDVATSQDDCY 381
QY 361 KEAISQSTGTVMGAVIMEGFYVFPDARKRIGFAVSACHVDEFTAAVEGPFYTLME 420
DB 382 KEAISQSTGTVMGAVIMEGFYVFPDARKRIGFAVSACHVDEFTAAVEGPFYTLME 441
QY 421 DCGYNIPQTDDEST 433
DB 442 DCGYNIPQTDDEST 454

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RESULT 12
US-09-795-847B-4
; Sequence 4, Application US/09795847B
; Patent No. 6753163
; GENERAL INFORMATION:
; APPLICANT: Gurney, Mark E.
; APPLICANT: Bienkowski, Michael J.
; APPLICANT: Heinrikson, Robert L.
; APPLICANT: Parodi, Luis A.
; APPLICANT: Yan, Ridiang
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/62808
; CURRENT APPLICATION NUMBER: US/09/795,847B
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0

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SEQ ID NO 4
 LENGTH: 501
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-795-847B-4

Query Match 99.1%; Score 2267; DB 4; Length 501;
 Best Local Similarity 99.1%; Pred. No. 1.3e-235;
 Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 TGHGRLPLRSGLGAPLGLINLETDEBEPGRGRGSFVEMVNDLRKSGGGYVEMTV 60
 22 TGHGRLPLRSGLGAPLGLRLPRETDEBEPGRGRGSFVEMVNDLRKSGGGYVEMTV 81
 61 GSPPTLNLIVDTGSSNFAVGAAPHPFLHRYQRLSSTYRDLRKGVVYPYTGKMEGL 120
 82 GSPPTLNLIVDTGSSNFAVGAAPHPFLHRYQRLSSTYRDLRKGVVYPYTGKMEGL 141
 121 GTDLVSIHPGNVTVRANIAAITSBDFKFFINGSNMEGILGLAYAEIARPDSDLLEPFDL 180
 142 GTDLVSIHPGNVTVRANIAAITSBDFKFFINGSNMEGILGLAYAEIARPDSDLLEPFDL 201
 181 VKQTHVPMFLSLQCGAFPLNOSVLA SVGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
 202 VKQTHVPMFLSLQCGAFPLNOSVLA SVGSMIIIGIDHSLYTGSLMYTPIRREMYE 261
 241 VIVVEINGODLKMDCKEYNDKSI VDSGTTNLRPKKVFEEAAVKSIIKAASSTKFPDG 300
 262 VIVVEINGODLKMDCKEYNDKSI VDSGTTNLRPKKVFEEAAVKSIIKAASSTKFPDG 321
 301 FWLGEQLVCWQAGTTPMNI FVVISLYLMGEVTVNOSFRITILPOQYLRPEVEDVATSQDDCY 360
 322 FWLGEQLVCWQAGTTPMNI FVVISLYLMGEVTVNOSFRITILPOQYLRPEVEDVATSQDDCY 381
 361 KFAISQSSGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEPRTAAVSGPFTLDME 420
 382 KFAISQSSGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEPRTAAVSGPFTLDME 441
 421 DCGYNIPTDST 433
 442 DCGYNIPTDST 454

RESULT 13

US-09-548-366F-4
 Sequence 4, Application US/09548366F
 Patent No. 6797487

GENERAL INFORMATION:
 APPLICANT: GURNEY ET AL.
 TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES THEREOF
 FILE REFERENCE: 29915/6280J
 CURRENT APPLICATION NUMBER: US/09/548,366F
 CURRENT FILING DATE: 2000-04-12
 PRIOR APPLICATION NUMBER: US 60/155,493
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: US 09/404,133
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: PCT/US99/20881
 PRIOR FILING DATE: 1999-09-23
 PRIOR APPLICATION NUMBER: US 60/101,594
 PRIOR FILING DATE: 1998-09-24
 NUMBER OF SEQ ID NOS: 73
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 4
 LENGTH: 501
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-548-366F-4

Query Match 99.1%; Score 2267; DB 4; Length 501;
 Best Local Similarity 99.1%; Pred. No. 1.3e-235;
 Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 TGHGRLPLRSGLGAPLGLINLETDEBEPGRGRGSFVEMVNDLRKSGGGYVEMTV 60
 22 TGHGRLPLRSGLGAPLGLRLPRETDEBEPGRGRGSFVEMVNDLRKSGGGYVEMTV 81
 61 GSPPTLNLIVDTGSSNFAVGAAPHPFLHRYQRLSSTYRDLRKGVVYPYTGKMEGL 120
 82 GSPPTLNLIVDTGSSNFAVGAAPHPFLHRYQRLSSTYRDLRKGVVYPYTGKMEGL 141
 121 GTDLVSIHPGNVTVRANIAAITSBDFKFFINGSNMEGILGLAYAEIARPDSDLLEPFDL 180
 142 GTDLVSIHPGNVTVRANIAAITSBDFKFFINGSNMEGILGLAYAEIARPDSDLLEPFDL 201
 181 VKQTHVPMFLSLQCGAFPLNOSVLA SVGSMIIIGIDHSLYTGSLMYTPIRREMYE 240
 202 VKQTHVPMFLSLQCGAFPLNOSVLA SVGSMIIIGIDHSLYTGSLMYTPIRREMYE 261
 241 VIVVEINGODLKMDCKEYNDKSI VDSGTTNLRPKKVFEEAAVKSIIKAASSTKFPDG 300
 262 VIVVEINGODLKMDCKEYNDKSI VDSGTTNLRPKKVFEEAAVKSIIKAASSTKFPDG 321
 301 FWLGEQLVCWQAGTTPMNI FVVISLYLMGEVTVNOSFRITILPOQYLRPEVEDVATSQDDCY 360
 322 FWLGEQLVCWQAGTTPMNI FVVISLYLMGEVTVNOSFRITILPOQYLRPEVEDVATSQDDCY 381
 361 KFAISQSSGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEPRTAAVSGPFTLDME 420
 382 KFAISQSSGTVMGAVIMEGFYVFPDRARKRIGFAVSACHVDEPRTAAVSGPFTLDME 441
 421 DCGYNIPTDST 433
 442 DCGYNIPTDST 454

RESULT 14

US-09-949-016-6810
 Sequence 6810, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C1001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 6810
 LENGTH: 501
 TYPE: PRT
 ORGANISM: Human
 US-09-949-016-6810

Query Match 99.1%; Score 2267; DB 4; Length 501;
 Best Local Similarity 99.1%; Pred. No. 1.3e-235;
 Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

1 TGHGRLPLRSGLGAPLGLINLETDEBEPGRGRGSFVEMVNDLRKSGGGYVEMTV 60
 22 TGHGRLPLRSGLGAPLGLRLPRETDEBEPGRGRGSFVEMVNDLRKSGGGYVEMTV 81
 61 GSPPTLNLIVDTGSSNFAVGAAPHPFLHRYQRLSSTYRDLRKGVVYPYTGKMEGL 120
 82 GSPPTLNLIVDTGSSNFAVGAAPHPFLHRYQRLSSTYRDLRKGVVYPYTGKMEGL 141
 121 GTDLVSIHPGNVTVRANIAAITSBDFKFFINGSNMEGILGLAYAEIARPDSDLLEPFDL 180

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Db 142 GTDLVSIPIHGPVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPFDSL 201
QY 181 VKQTHVNLPSLQICGAGFPINQSEVTLASVGGSMIIGIDHSLYTGSLSMTPIRREWYE 240
Db 202 VKQTHVNLPSLQICGAGFPINQSEVTLASVGGSMIIGIDHSLYTGSLSMTPIRREWYE 261
QY 241 VVIYRVEINGDLMKDCKEVYDYSIDSGTTNLRPKVFEAAVSIKAASTKPEPC 300
Db 262 VVIYRVEINGDLMKDCKEVYDYSIDSGTTNLRPKVFEAAVSIKAASTKPEPC 321
QY 301 FWLGEOLVCWQAGTTPNNIFPVISLYLMGEVTNQSFRITILPOQYLRPVEDVATSODDCY 360
Db 322 FWLGEOLVCWQAGTTPNNIFPVISLYLMGEVTNQSFRITILPOQYLRPVEDVATSODDCY 381
QY 361 KFAISQSTGTVMGAVIMEGFYVFDRAKRIGFAVSACHVDEFRTAAVEGPFVTLME 420
Db 382 KFAISQSTGTVMGAVIMEGFYVFDRAKRIGFAVSACHVDEFRTAAVEGPFVTLME 441
QY 421 DCGYNIPTDEST 433
Db 442 DCGYNIPTDEST 454
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RESULT 15
US-09-548-368D-4
; Sequence 4, Application US/09548368D
; Patent No. 6825023
; GENERAL INFORMATION:
; APPLICANT: GURNEY ET AL.
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
; FILE REFERENCE: 29915/6280C
; CURRENT APPLICATION NUMBER: US/09/548,368D
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-548-368D-4
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Query Match 99.1%; Score 2267; DB 4; Length 501;
Best Local Similarity 99.1%; Pred. No. 1,3e-235;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 TOHGIRLPKRSGLGAPLGLINLETDEPERGRGSPVEMDNLRKSGCGYIVEMTV 60
Db 22 TOHGIRLPKRSGLGAPLGLRPRETDEPERGRGSPVEMDNLRKSGCGYIVEMTV 81
QY 61 GSPPTNLIVDTGSSNFAVGAAHPFLHRYQROLSTYRDLKGVVVPYTOGKEGEL 120
Db 82 GSPPTNLIVDTGSSNFAVGAAHPFLHRYQROLSTYRDLKGVVVPYTOGKEGEL 141
QY 121 GTDLVSIHGPVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPFDSL 180
Db 142 GTDLVSIHGPVTVRANIAAITESDKFFINGSNWEGILGLAVAEIARPDLSLEPPFDSL 201
QY 181 VKQTHVNLPSLQICGAGFPINQSEVTLASVGGSMIIGIDHSLYTGSLSMTPIRREWYE 240
Db 202 VKQTHVNLPSLQICGAGFPINQSEVTLASVGGSMIIGIDHSLYTGSLSMTPIRREWYE 261
QY 241 VVIYRVEINGDLMKDCKEVYDYSIDSGTTNLRPKVFEAAVSIKAASTKPEPC 300
Db 262 VVIYRVEINGDLMKDCKEVYDYSIDSGTTNLRPKVFEAAVSIKAASTKPEPC 321
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QY 301 FWLGEOLVCWQAGTTPNNIFPVISLYLMGEVTNQSFRITILPOQYLRPVEDVATSODDCY 360
Db 322 FWLGEOLVCWQAGTTPNNIFPVISLYLMGEVTNQSFRITILPOQYLRPVEDVATSODDCY 381
QY 361 KFAISQSTGTVMGAVIMEGFYVFDRAKRIGFAVSACHVDEFRTAAVEGPFVTLME 420
Db 382 KFAISQSTGTVMGAVIMEGFYVFDRAKRIGFAVSACHVDEFRTAAVEGPFVTLME 441
QY 421 DCGYNIPTDEST 433
Db 442 DCGYNIPTDEST 454
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Search completed: August 22, 2005, 00:26:27
Job time : 67 sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2005, 00:25:14 ; Search time 5781 Seconds
(without alignment)
2851.034 Million cell updates/sec

Title: US-10-726-967a-84

Perfect score: 2288

Sequence: 1 TGHGIRLPURSGLGAPLGL.....FTYLDMEGCVINPQTDST 433

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Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 3423544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-O=sgn2.1/USPTO.spool.p/US10726967/runat.19082005.201240.29636/app_query.fasta_1.583
-DB=EST -OPMT=faetap -SUFPRX=tbl -MINMATCH=0.1 -LOOPEC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=diolune2 -TRANS=human40.cdi -LIST=45
-DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10726967 @CGN.1.1.5180 @runat.19082005.201240.29636 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2267	99.1	1506	9 AY417360	Homo sapi
2	2222	97.1	1445	9 AY417361	Pan trogl
3	2216	96.9	1506	9 AY417362	Mus muscu
4	2216	96.9	3634	3 AK041285	Mus muscu
5	2216	96.9	3859	3 AK014464	Mus muscu
6	2216	96.9	3877	3 AK031112	Mus muscu
7	2215	96.8	4046	3 AK049626	Mus muscu
8	2211	96.6	4101	3 AK046175	Mus muscu
9	2189	95.7	3880	3 AK080498	Mus muscu

10	2181	95.3	3805	3 AK082230	Mus muscu
11	2023	88.4	4048	3 AK082317	Mus muscu
12	1537	67.2	3147	3 AK079814	Mus muscu
13	1425	62.3	928	5 BUS57282	AGENCOURT
14	1375.5	60.1	1001	5 BU128383	AGENCOURT
15	1365	59.7	950	5 BU502697	AGENCOURT
16	1364	59.6	802	5 BU613719	UI-M-EWO
17	1315.5	57.5	846	7 CK021791	AGENCOURT
18	1273.5	55.7	926	5 BX433493	BX433493
19	1257	54.9	862	4 B1157614	602922587
20	1240.5	54.2	813	7 CN224123	WLA053B12
21	1163	50.8	2504	3 AK014390	Mus muscu
22	1158.5	50.6	720	4 BG288435	602383404
23	1136	49.7	1968	3 CR622762	UI-M-1eng
24	1135	49.6	840	2 BB885725	601508937
25	1122	49.0	836	7 CO382805	AGENCOURT
26	1120	49.0	3703	3 AK078770	Mus muscu
27	1115	48.7	1810	3 AK052309	Mus muscu
28	1100.5	48.1	730	4 BM048418	603625683
29	1099	48.0	631	7 CFS39391	UI-M-GHO-
30	1093	47.8	624	5 BU708350	UI-M-FCO-
31	1048	45.8	1114	1 AF150387	AF150387
32	1036	45.3	684	1 AV725513	AV725513
33	1036	45.3	904	2 BE378929	601237528
34	1007	44.0	808	7 CK833062	4056853 B
35	1005.5	43.9	633	5 BU073919	1n26c07.Y
36	997	43.6	789	2 BF204338	601666411
37	992	43.4	635	2 BE296749	601175134
38	972	42.5	797	5 BU193314	AGENCOURT
39	956.5	41.8	605	2 BE793449	601588510
40	954	41.7	826	5 BU182102	AGENCOURT
41	941	41.1	562	6 BY713531	K0314H01-
42	923	40.3	529	6 CA563516	AV667139
43	912	39.7	542	1 AV667139	601868788
44	907.5	39.9	939	2 BF203806	601868788
45	892	39.0	513	5 BQ637035	he04912.Y

ALIGNMENTS

RESULT 1
AY417360
LOCUS
DEFINITION
Homo sapiens BACE gene, 1506 bp DNA linear GSS 17-DEC-2003
ACCESSION
AY417360
VERSION
AY417360.1 GI:39773320
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 (bases 1 to 1506)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

TITLE

JOURNAL
Science 302 (5652), 1960-1963 (2003)

PUBMED
14671302
2 (bases 1 to 1506)
REFERENCE
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Substitution
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

JOURNAL

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
1. 1506

FEATURES
source

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/db_xref="taxon:9606"
<1..>1506
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ORIGIN

Alignment Scores:

Pred. No.: 1.2e-245 Length: 1506
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: Gaps: 0

US-10-726-967a-84 (1-433) x AY117360 (1-1506)

QY 1 ThTGLNHISGLIYIARGLLEUPROLEUARGSERGLYLEUGLYALAPROLEUGLYLEU 20
DB 64 ACCAGACGCGCATCCGGCTGCCCTGCGACGGGGCTGGGGGGCCCCCTGGGGCTG 123
QY 21 GLIULEANLEUGLUTIRAPGLUGLUPROGLUGLUPROGLYARGLYSERPHEVA 40
DB 124 CGGCTGCCGGGAGACCGACGAGGCCCGAGAGCCCGCGGAGGGGCGAGCTTTGTG 183
QY 41 GLUMETVALAPBANLEUARGLYLYSERGLYGLINGLYTYRTYRVALGIMETTHRVA 60
DB 184 GAGATGGTGAACAACCTGAGGGGCGACAGTCCGGGCTACTACGAGATGACCGTG 243
QY 61 GLYSETPROPROGLINTHLEUANILLEUVALASPETHGLYSESERANPHEALVA 80
DB 244 GGCAGGCCCGCGAGACGCTCAACATCTGTGTGATACAGGACGACGATCTTGACGTG 303
QY 81 GLYVALAPROHISPROPHLEUHSARGTYRTYRGLAARGGLNEUSERSETHRTYR 100
DB 304 GGTGCTGCCCCCAACCCCTTCTGTGATCGCTACTACAGAGGAGGTGTCCAGCACATAC 363
QY 101 ARGAPLEUARGLYSGLYVALTYRVALPROTYRTHGLINGLYLSTRTPLUGLUGLEU 120
DB 364 CGGACCTCCGGAGGGGTGTGTGTGCCCTACACCGAGGGAGAGGGAGGAGCTG 423
QY 121 GLYTHAPLEUVALSERILEPROHISGLYPROBANVALTHVALARGALANILLEA 140
DB 424 GGCACGACCTGTGATGATCCGCCACATGCGCCCAACGTACGTGCTGCCAACATTCCT 483
QY 141 ALAILETHGLUSERAPLYSPHEPHEILEANGLYSERANTRPGLUGLYLLEUGLY 160
DB 484 GCCATCACTGAGTACAGACAGATTCTTCATCAACGGCTCCACCTGGAGAGGACATCTGGGG 543
QY 161 LEUVALTYRVALGLULEALARGPROAPAPSERLEUGLUPROPHENAPSERLEU 180
DB 544 CTGGGCTTATGTGAGATTGCCAGGCTCGACCTCCCTGAGACCTTTCTTGACCTCTG 603
QY 181 VALLYSGINTHPIHISVALPROBANLEUPHESERLEUGLNEUCYSGLYVALGILPHEPRO 200
DB 604 GTAAAGACAGACCCAGCTTCCCAACCTCTTCTCCGACGCTTTGGTGGCTGCTTCCC 663
QY 201 LEUANGINSEGLIUALLEUVALSERVALGILYISERMELLEIGLYLLEASP 220
DB 664 CTCACACAGTCTGAGTGTGCTCTGTGCGAGGGAGACATGATTCATTCGAGATTCAC 723
QY 221 HISSELEUTYRTHGLYSERLEUTRPLYRTHPROLLIEARGAGLUTTPYRTYRGLU 240
DB 724 CACTGCTGTACACAGGAGCTCTGTGTATACACCCATCCGCGGAGTGTATTATAGAG 783
QY 241 VALLEILEVALARGVALGILLEANGLYGINAPLEULYSMETLAPCYVALGILUTYR 260
DB 784 GTGATCATTTGCGGGTGGAGATCAATGACAGGATCTGAAATGAGATCGACAGAGAC 843
QY 261 ASNTYRAPPYLSERILEVALAPSERGLYTHRTHANLEUATGLEUPROLYSVAL 280
DB 844 AACTATGACAGAGCATGTGTGACAGTGGACCAACCACTTTCGTTTCCCAAGAAAGTG 903

QY 281 PHEGUALAALAYLSESERILEYVALAASESERTHRGILYSPHEPROASPGLY 300
DB 904 TTTGAAGCTGACAGTCAAAATTCATCAAGGACACCTCTCTCCAGGAAAGTTCCGTGATGCT 963
QY 301 PHETPLEUGLYGLUGLLEUVALCYSTRPOLNALAGLYTHRTHPROTPANILLEPHE 320
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QY 321 PROVALILESERLEUTYRLEUMERGILYGLIUALTHRANGINSESPHEARGILIE 340
DB 1024 CCAGTCATCTACTTCACTTAACTTAATGGGTGAGTTTCAACACAGTCTTCCGATCAACATC 1083
QY 341 LEUPROGLINGLYRLEUARGPROVALGLUAPVALAATHRSESGINAPASPCTYR 360
DB 1084 CTTCGCGACAAATCTGTGCGGCGCAGTGGAAGATGTGGCCACAGTCCCAAGACGACTGTAC 1143
QY 361 LYSPPHEALAILESERGINSESERTHRGLYTHRVALIMETGLYVALIILEMETGLUGLY 380
DB 1144 AAGTTTGCATCTCACTCACTATCCAGCGACCTGTATAGGAGCTGTATCATGAGAGGC 1203
QY 381 PHETYRVALVALPHEAPARGALAAARGLYSARGILEGLYPHEALVALSERALA 400
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QY 401 VALHISAPGLUPHEAHTGTHRALAALVALGLUGLYPROBHEVALTHLEUAPMETGLU 420
DB 1264 GTGCACAGATGATTCACAGACGCGCAGCGGTGGAAGCCCTTTGTGTCACTTGACATGAA 1323
QY 421 ASPCYSGLYTYRANILLEPROGLINTHFAAPGLUSERTHR 433
DB 1324 GACTGTGGCTTACAAATTCACACAGACAGATGATCAACC 1362

RESULT 2
AY117361 1445 bp DNA linear GSS 17-DEC-2003
LOCUS
DEFINITION
Pan troglodytes BACE gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
AY117361
AY117361.1 GI:39773321
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1 (bases 1 to 1445)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
2 (bases 1 to 1445)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
1..1445
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/mol_type="genomic DNA"
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<1..>1445
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ORIGIN

Alignment Scores:

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 Score: 2222.00 Matches: 422
 Percent Similarity: 97.69% Conservative: 1
 Best Local Similarity: 97.46% Mismatches: 10
 Query Match: 97.12% Indels: 0
 DB: 9 Gaps: 0

US-10-726-967a-84 (1-433) x AY417361 (1-1445)

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 DB 8 ACCGAGCAGCGGATCCGGCTGCCNNNNNNACGGGGCTGGGNNNGCCCCCTGGGGCTG 67
 QY 21 GluIleamLeuGlyThraSpGluGluProGluGluProGlyAraGrglySerPheVal 40
 DB 68 CGGCTGCCCCGGAGACCGACAGAGGCCGAGAGCCCCGGCCGAGGGGCAAGCTTTGG 127
 QY 41 GluMetValAspAsnLeuArglyGlySerGlyGlnGlyYrYrValGluMetThrVal 60
 DB 128 GAGATGTGTGACAACTGAGGGCAAGTCGGGGCAGAGNCTACTACGTGAGATNNNCTG 187
 QY 61 GlySerProGlnThraLeuamIleleuValAspThrGlySerSerPheAlaVal 80
 DB 188 GGCAGCANNCCCCGACGCTCAACATCTGGTGATACAGGACGACGATCTTGGAGTG 247
 QY 81 GlyAlaAlaProHisProPheLeuHisArgYrYrGlyAraGlyLeuSerSerThrYr 100
 DB 248 GGGTGTGCCCCCAACCCCTTCTGTCATCGCTACTACAGGACGCTGTCCAGCACATAC 307
 QY 101 ArgAspLeuArglyGlyValYrYrValProYrYrThraGlnGlyYrYrGluGlyLeu 120
 DB 308 CGGAGCTCCGAGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 367
 QY 121 GlyThrAspLeuValSerIleProHisArgYrProAsnValThrValArgAlaAsnIleAla 140
 DB 368 GGCACCGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 427
 QY 141 AlaIleThraGlnSerAspAspPhePheIleamGlySerAsnTrpGluGlyIleGluGly 160
 DB 428 GGCATACATGAAACAGACAGATTTCTTCTATCAACGGCTCCACTGGAGAGCATCTGGGG 487
 QY 161 LeuAlaYrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
 DB 488 CTGGCCTTAATGCTGAGATTGCTGCAAGCTGACGATCTCCCTGGAGGCTTTCTTGACTCTG 547
 QY 181 ValIleGlnThraHisValProAsnLeuPheSerLeuGlnLeuCyArglyAlaGlyPhePro 200
 DB 548 GTAAACAGACCCCAAGCTTCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 607
 QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
 DB 608 CTCACACAGCTGTAAGTGTGGCTCTGTCTGTGGAGGAGCATGATCTTGGAGGATTCGAC 667
 QY 221 HisSerLeuYrThraGlySerLeuTrpYrThraProIleArgArgGluTrpYrYrGlu 240
 DB 668 CATTCCTGTACACAGGAGCTCTGCTATACACCATTCGGGGGAGGTGTATTATAG 727
 QY 241 ValIleIleValArgValGluIleamGlyGlnAspLeuYMetAspCyArglyGluTrp 260
 DB 728 GTGATCATGTGTGGGGTGTGATCAATGACAGAGATCTGAAATATGACCTGCAAGAGGTAC 787
 QY 261 AsnYrAspAspSerIleValAspSerGlyThraAsnLeuArgLeuProYrYrVal 280
 DB 788 AACATATGACAAAGCATTTGTGACAGTGGACCAACCACTTGTTGGCCCAAGAAAGTG 847
 QY 281 PheGluAlaIleValIleYrSerIleYrAlaIleSerSerThraGluYrPheProAspGly 300
 DB 848 TTGTGAGCTGCAAGTCAATCAATCAAGGAGGCTCTCCCAAGAGAAATTCCTGATGAT 907
 QY 301 PheTrpLeuGlyGluGlnLeuValCyTrpGlnAlaGlyThraProTrpAsnIlePhe 320

DB 908 TTCTGCTAGAGAGACAGCTGATGTGTGCAAGCGGACACACCCTTGGAAATTTTC 967
 QY 321 ProValIleSerLeuYrLeuMetGlyGluValThraGlnSerPheArgIleThrIle 340
 DB 968 CCAGTCACTCACTTACTTATGTGGTGTACCAACAGTCTCTCCGATCACCATC 1027
 QY 341 LeuProGlnGlnYrLeuArgProValGluAspValAlaThrSerGlnAspAspCyTrp 360
 DB 1028 CTTCCGACATACCTCGGCGCAGTGAAGATGTGGCCAGCTCCCAAGACAGCTTAT 1087
 QY 361 LysPheAlaIleSerGlnSerSerThrGlyThraValMetGlyAlaValIleMetGluGly 380
 DB 1088 AAGTTGCACTTCACTCACTTCACTCACTGAGCTGTATGAGAGCTGTATATCAGAGGAC 1147
 QY 381 PheYrValIleValPheAspArgAlaArgYrArgIleGlyPheAlaValSerAlaCyTrpHis 400
 DB 1148 TTCTAGCTGTGTCTTGTGATCGGGCCGAAAGAAATGTGCTTTGCTGTACGCGCTTGCAAT 1207
 QY 401 ValHisAspGluPheArgThraAlaAlaValGluGlyProPheValThraAspMetGlu 420
 DB 1208 GTGCAGATGACTTACAGACGGCAGCGGTGAGAGCCCTTTGTTCACCTTGGACATGGAA 1267
 QY 421 AspCyGlyYrYrAsnIleProGlnThraAspGlnSerThr 433
 DB 1268 GACTGTGGCTACAACTTCCACAGACAGATGATCAACC 1306
 RESULT 3
 AY417362 1506 bp DNA linear GSS 17-DEC-2003
 LOCUS Mus musculus BACE gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY417362.1 GI:39773322
 VERSION AY417362.1 GI:39773322
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1506)
 Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 AUTHORS Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civeallo,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Snihsy,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
 FEATURES
 source
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 /mol_type="genomic DNA"
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 /gene="BACE"
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 ORIGIN
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 Score: 2216.00 Matches: 418
 Percent Similarity: 97.69% Conservative: 5
 Best Local Similarity: 96.54% Mismatches: 10
 Query Match: 96.85% Indels: 0

DB: 9 Gaps: 0

US-10-726-967a-84 (1-433) x AY417362 (1-1506)

QY 1 ThGlnHISGlyIleArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20

DB 64 ACCATCTCGGCATCCGGCTGCCCTTCCGACGGCTGGCAAGGCCACCCCTGGGCTG 123

QY 21 GluIleuLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40

DB 124 AGGCTGGCCCGGAGACCGACGAGAGAAATCGAGAGAGCTGCGCGAGAAAGCACCTTTGTTG 183

QY 41 GluMetValAspPheLeuArgGlyLeuSerGlyGlnGlyTyrTyrValGluMetThrVal 60

DB 184 GAGATGTGACAACTCGAGGGGAAAGTCCGAGCCAGGGCTACATGTGGAGATGACCGTA 243

QY 61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySerSerPheAsnIleVal 80

DB 244 GCGAGCCCCCAGACGCTCAACATCTGTGGAGACGGGAGTGTAACTTTGGACGTG 303

QY 81 GlyAlaIleAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100

DB 304 GGGGCTGCCCCACACCTTCTTCGACATCGCTACTACCAAGGACGCTGTCACACATAT 363

QY 101 ArgAspLeuArgGlyGlyValTyrValProTyrThrGlnGlyTyrTrpGluGluLeu 120

DB 364 CGAGACCTCCGAAAGGGGTGTATGTCTTACACCCAGGGGCAAGTGGAGGGGAACTG 423

QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140

DB 424 GGGACGACCTGTGTGACATCCCTCATGGCCCCCAAGCTCATGTGCGTCCAAATTTGCT 483

QY 141 AlaIleThrGlySerAspLeuPhePheIleAsnGlySerAsnThrGluGlyIleLeuGly 160

DB 484 GCCATCACTGAAACCGACAAAGTTCTTCAATGATGTTCCAACTGGGAGGCAATCTTGA 543

QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180

DB 544 CTGGCTATGTCTGAGATTGGCAGGCCGAGACCTCTTGGAGCCCTTCTTAACTCCCTG 603

QY 181 ValIleGlnThrHisAlaProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro 200

DB 604 GTGAACCAAGCCACCAATCTTCCCAACATCTTCCCTGACCTGTGGCCCTGCTTCCCC 663

QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlySerMetIleIleGlyGlyIleAsp 220

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QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240

DB 724 CACTGCTATACACGGGAGCTCTGTGTACACACCATCCGCGGAGTGTATTATGAA 783

QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuMetAspCysLeuGlyIle 260

DB 784 GTGATCATTTGTCGCTGGAATTCATAGTCAAGATCTCAAGATGACTCGAAGGAGATC 843

QY 261 AsnTyrAspLeuSerIleValAspSerGlyThrThrAsnLeuArgLeuProGlyIleVal 280

DB 844 AACTACGACAAAGACATTGTGACAGTGGGACCAACCACTTCCTGCCCAAGAAAGTA 903

QY 281 PheGluAlaAlaValIleSerIleGlyAlaAspSerThrGluLeuPheProAspGly 300

DB 904 TTTGAGAGCTGCGGTACATGCTCAAGGACAGCTCTCGACGAGAAATGTCCTCGGATG 963

QY 301 PheTyrPheGluGlyGluIleuValCysTrpGlnIleGlyThrThrProTyrAsnIlePhe 320

DB 964 TTTTGGCTAAGGGAGACAGTGTGTGTGGACAGGACAGACACCTTGGAAACATTTTC 1023

QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340

DB 1024 CCAGTCATTTACCTTACCTCATGGGTGAAGTCAACATCATGCTTCCGATACCATC 1083

QY 341 LeuProGlnGlnTyrLeuArgProValGluIleAspValAlaThrSerGlnAspAspCysTyr 360

DB 1084 CTTCCTCGACATATACCTACGGCCGGTGGAGAGACGGGCCACGTCCCAAGACGATTTAC 1143

QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380

DB 1144 AAGTTCGCTGCTTCACAGTCAATCCAGGGCACTGTATTAAGGAGCCGTATCATGAAAGT 1203

QY 381 PheTyrValIlePheAspArgAlaArgIleAspArgIleGlyPheAlaValSerAlaCysHis 400

DB 1204 TTCTATGTGCTCTTCATCGACGAGCCGAAAGCGAATTTGCTGTCTCAAGCGCTTGCCAT 1263

QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420

DB 1264 GTGCAGATGATTCAGACGCGCGCAGTGGAAGTCCGTTGTTCACGCGACATCGAA 1323

QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433

DB 1324 GACTGTGCTACAACTTCCCAAGACAGATGATCAACA 1362

RESULT 4
AK041285
LOCUS
DEFINITION
AK041285 3634 bp mRNA linear HTC 03-Apr-2004
Mus musculus adult male aorta and vein cDNA, RIKEN full-length
enriched library, clone:A530097B07 product:beta-site APP cleaving
enzyme, full insert sequence.
ACCESSION
AK041285
VERSION
AK041285.1 GI:26334342
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS
Carninci, P. and Hayashizaki, Y.
TITLE
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNALS
MEDLINE
PUBMED
99279253
10349636
REFERENCE
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Komano, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE
Normalization and subraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
JOURNALS
MEDLINE
PUBMED
20499374
11042159
REFERENCE
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Komano, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsubara, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNALS
MEDLINE
PUBMED
20530913
11076861
REFERENCE
AUTHORS
The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
TITLE
Functional annotation of a full-length mouse cDNA collection
JOURNALS
MEDLINE
PUBMED
11076861
REFERENCE
AUTHORS
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNALS
MEDLINE
PUBMED
120530913
11076861
REFERENCE
AUTHORS
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katch, H., Kawai, D., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsao, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shidato, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://fantom.gsc.riken.jp/
URL: http://genome.gsc.riken.jp/

FEATURES

source

CDS

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AAITSDKFPINGSNWEGILGLAVAIAPDLSLBPFPGLVQTHIPNIFSLQCGA
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VMGAVIMEGTVVFDRAKRI.GFVSAACHDEFRFAVYEGPFTVMDMDCGNITPOT
DESTLMTIYVMAI.CALF.MLP.LCLMV.CQRC.LRCLRHODHDFADDISLKL"

ORIGIN

Alignment Scores:

Pred. No.: 2.9e-239 Length: 3634
Score: 2216.00 Matches: 418
Percent Similarity: 97.69% Conservative: 5
Best Local Similarity: 96.54% Mismatches: 10
Query Match: 96.85% Indels: 0
DB: 3 Gaps: 0

US-10-726-967a-84 (1-433) x AK041285 (1-3634)

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Qy 41 Gluilevalappasnleuargglylyserglyglnghlytyrtyrvalgluwerthrval 60
Db 633 GAGAGGTGGGCAACCTTAGGGGAAAGTCGCGGCGGCTCTATGTAGATGACCGTA 692
Qy 61 Glyserproproglnthrluasnlleuvalaspthrglyseraserasnphela1val 80
Db 693 GGCACCCCCCAACAGACCTCAACATCTGGTGGACACGGCAGTACATCTTGCACATG 752
Qy 81 Glyala1aprohisprophleuuhlsargtyrtyrglnarglnleuserthrtyr 100
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Qy 101 Argappaleuaglyglyvaltyrtyr1protyrthrghnglylysertrglnghlyglnleu 120
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Qy	421	AAspCyGeG1YTYrAmnIleProGlnTHrAspGuseTrHr	433
Db	1773	GACTGTGGCTACACACTTCCCCAGACAGTAGTGTCACA	1811
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LOCUS	AK014464	3859 bp mRNA linear HTC 03-APR-2004	
DEFINITION	AK014464	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:4122401C04 product:beta-site APP cleaving enzyme, full insert sequence.	
ACCESSION	AK014464		
VERSION	AK014464.1	GI:12852334	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;		
AUTHORS	Carninci, P., and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komoto, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
PUBMED	20499374		
REFERENCE	11042159		
AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagasaki, S., Saeki, N., Carninci, P., Komoto, H., Akiyama, J., Nishi, K., Kitamura, T., Tashtiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nabhitte, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Itawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
PUBMED	20530513		
REFERENCE	11076861		
AUTHORS	4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
PUBMED	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
REFERENCE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
AUTHORS	Nature 420, 563-573 (2002)		
TITLE	6 (bases 1 to 3853)		
JOURNAL	Aadachi, J., Aizawa, K., Akahita, S., Akimura, T., Arai, A., Aono, H., Adakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Horii, P., Imotani, K., Ishii, Y., Itoh, M., Itawa, M., Kanakawa, T., Kato, H., Kawai, J., Koijima, Y., Komoto, H., Kouda, M., Koyas, S., Kuhihara, C., Matsuyama, T., Miyazaki, A., Nishik, K., Nomura, K., Numezaki, R., Oho, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, P., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamatsuta, M., and Hayashizaki, Y.		

TITLE
JOURNAL

Submitted (10-Jul-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama kangawa 230-0045, Japan (E-mail: genome-res@gscl.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGAAGAAATCCCAAGACTCTTTTTCCTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adaptor of sequence [5' GAGGAGAAGATTCTCGAGTTAATTAATTAATACCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified plasmidscript KS(+/-) after bulk excision from lambda PLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B

FEATURES

source

Location/Qualifiers

1..3859

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/db_xref="taxon:T0090"

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/tissue_type="head"

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/dev_stage="16 days embryo"

430..._1935

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ORIGIN

Alignment Scores:

Pred. No.: 3.19e-239 Length: 3859

%Ident: 2216.00 Matches: 418

Percent Similarity: 97.69% Conservative: 5

Best Local Similarity: 96.54% Mismatch: 10

Diver Match: 96.85% Indels: 0

Gaps: 3 0

US-10-726-967A-84 (1-433) x AKO14464 (1-3859)

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QY 21 GlutAsnLeuLjuthrArpGlugluProgluGluProgluValArgArgGlysereVal 40

Bd 553 AGCGTCGCCGGAGACCGACGGAATRGAGAGAACCTCGGCGGAGAGGCACTTTGTG 612

Zy 41 GluMetValAspaNdeulaTgilylYserGylnglyTytyrTyrAlaGluMetThrval 60

Db 613 GAGATGATGACACCTGAGGGGAAAGTCGGGCGAGGCTACTATGAGATGACCTGTA 672
 Oy 61 G1ySerProGlnThrLeuAen11eLeuValAapThrglySerSerAanphea1aVal 80
 Db 673 GGCACCCCCCACAAGACGCTCAACATCCGTGTGACACGGGACAGTAAGTAACCTTCAGAG 732
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 Oy 101 ArgAapLeuAarglyGlyVal1yTyrVal1yPro1yTyrThrgln1yTyrGln1y 120
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 Db 853 GGCACCGACCTGTGTAGCATCCCTCAATGGCCCCCAAGCTCACTGTGTGCCAATTCCT 912
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 Db 973 CTGGCCTATGCTGAAGATTGCCAGGCCCAAGCATCTTTGAGACCTCTTTTAACTCCCTG 1032
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 Db 1213 GGTATATGTATGATGTTGAAATCAATGTGTCAAGATCTCAAGATGACATGCAAGAGTAC 1272
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 RESULT 6
 AK033112
 LOCUS
 DEFINITION
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 AK033112
 AK033112.1 GI:26328834
 HTc; CAP trapper.
 Mus musculus (house mouse)
 SOURCE
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ORGANISM
 ACCESSION
 VERSION
 KEYWORDS
 REFERENCES
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349636
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
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 11042159
 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Teshiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, S., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wakahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
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 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)
 5 The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3877)
 Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirao, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, D., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.

FEATURES

source

1. 3877

Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 3, 21e-239 Length: 3877
Score: 2216.00 Matches: 418
Percent Similarity: 97.69% Conservative: 5
Best Local Similarity: 96.54% Mismatches: 10
Query Match: 96.85% Indels: 0
DB: 3 Gaps: 0

US-10-726-967a-84 (1-433) x AK031112 (1-3877)

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21 GtUleAsnLeuGluThrAAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
573 AGGCTGCGCCCGGAGACGCGAGAAATCGAGAGAGCTGCGCGAGAGGACGCTTTGTG 632
41 GtUmetValAAspAsnLeuArgGlySerGlyGlnGlyTyrTyrValGtUmetThrVal 60
633 GAGATGGTGGACAACTGAGGGGAAAGTCGCGCCAGGCGCTACTGTGTGAGATGACCGTA 692
61 GlySerProGluThrLeuAsnIleLeuValAAspThrGlySerSerAAspAlaVal 80
693 GGCACCCCCCAGACGCTCAACATCTTGTTGACAGCGGACAGTAACTTTCGAGTG 752
81 GtYAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
753 GGGGCTGCCCAACACCTTCTCTGATGCTACTACGACGAGAGCGAGCTGTCCAGCACATAT 812

101 ArgAAspLeuArgGlyValTyrValProTyrThrGlnGlyLeuTyrGluGlyLeu 120
813 CCAAGACCTCCGAAAGGAGTGTATGTGCTTCACACCCAGGCGCACTGGAGGGGAACTG 872
121 GtYThrAAspLeuValSerIleProHisGlyProAsnValThrValAArgAlaAsnIleAla 140
873 GGCACCGACCTGGTAGCATCCCTCATAGCCGCAACGTCAGTGGCGGCAACATGCT 932
141 AlaIleThrGluSerAAspLysPhePheIleAsnGlySerAsnTPGtUgIleLeuGly 160
933 GGCATCATGAAATCGACAAATGTTCTTCAATCAATGTTCCATGGAGGCGATCTTGGG 992
161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180
993 CTGGCTTATGCTGAGATTGGCAGAGCCGACGACACTTGTGAGCCCTTCTTGAATCCCTG 1052
181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
1053 GTGAAGCAGACCAATTCACCAACATCTTTCCTGACGCTGTGGCGCTGGCTCC 1112
201 LeuAsnGlnSerGluValLeuAlaSerValGlySerMetIleIleGlyGlyIleAsp 220
1113 CTCACCGACGACGAGGACCTGCTCGGTGGAGGAGCATGATCATGTTGGTATGAC 1172
221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
1173 CACTGCTATACAGGGCAGTCTCTGTACACACCCATCCGGCGGAGTGTATATGAA 1232
241 ValIleIleValAArgValGluIleAsnGlyValAAspLeuSerAspCysLysGluTyr 260
1233 GTGATCATTTGACCTGTGAAATCAATGTCAGATTCATCAAGATGACGCAAGAGATAC 1292
261 AsnTyrAAspLysSerIleValAAspSerGlyTyrThrAsnLeuArgLeuProLysVal 280
1293 AACTACGACAAAGCATTTGGGACAGTGGGACCAACCACTTGGCTTGGCCCAAGAAATG 1352
281 PheGluAlaAlaValLysSerIleLysAlaAlaSerSerThrGluLysPheProAspGly 300
1353 TTTAACTCTCGCAAGTCAATCAAGGACCTCTTCAAGGAGAAATGTCCTGGATGGC 1412
301 PheTyrPheGluGlyGluLeuValCysTyrGlnAlaGlyTyrThrProTyrAsnIlePhe 320
1413 TTTTGGCTAGGGAGGAGCAGTGTGCTGCGCAAGCAGCAGCAGCCTTGGAAATTTTC 1472
321 ProValIleSerLeuTyrLeuMetGlyValIleThrAsnGlnSerPheArgIleThrIle 340
1473 CCAATCAATTCACCTTAACCTCATGGGTGAAGTCAACCAATCAGTCTTCCGATCAACATC 1532
341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
1533 CTTCCTCAGCAATACCTTACGCGCGGTGAGAGAGTGGCCAGCGTCCCAACAGCATGTTC 1592
361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
1593 AAGTTCGCTGTCAAGTCAATCAGGAGCAGCTTATGAGGCGCGTATCATGGAAGGT 1652
381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
1653 TTTTATGTGTCTTCATGATGAGCGCCGAAAGCAATTTGGCTTGTGCTGACGCGCTTGCAT 1712
401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValIleLeuAspMetGlu 420
1713 GTGACGATGAGTTCAGAGCGGCGGAGAGTGAAGGTCCCTTGTATCCGCGACATGGA 1772
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1773 GACTGTGCTTACAAATTCGCCAGACAGATGATCAACA 1811

RESULT 7
AK049626 4046 bp mRNA linear HTC 03-APR-2004
LOCUS AK049626
DEFINITION Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length

Db	916	GCATCATCTGAATCGGACAGAGTCTTTCATCAATAGTGTCCAACTGGGAGGGCATCTCAAGG	973
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Db	976	CTGAGCTTAAGCTAGAGATTGGCAGGCCCGACGACTCTTTGGAGCCCTCTTTGACCTCCG	1035
Qy	181	ValIleGlnThrHisValProAlaLeuPheSerLeuGlnLeuCysGluValAlaIlePhePro	200
Db	1036	GTCAGACAGACCCACATCTCCCAACATCTTTCCCTGACACTCTTGAGCGCTGGCTTCCCC	1095
Qy	201	LeuAsnGlnSerGluValLeuAlaSerValGlyIleSerMetIleIleGlyIleIleAsp	220
Db	1096	CTCAACACGACCCGAGCAGCTGGCGCTCGTGGAGGAGCATGATCATTTGGTGTATCGAC	1155
Qy	221	HisSerLeuTyrThrGlySerLeuTyrPylTrpTrpProIleArgArgGluTrpTyrGlu	240
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Qy	261	AsnTyrAspLysSerIleValAspSerGlyTyrThrAsnLeuArgLeuProLysVal	280
Db	1276	AACCTACGACAAAGCATTTGTGACAGTGGACACCAACCTTCGCTTCCCAAGAAAGTA	1335
Qy	281	PheGluAlaAlaValAlaLysSerIleLysAlaAlaSerSerThrGluLysPheProAspGly	300
Db	1336	TTTGAAGCTGGCGTCAAGTCCATCAAGCAGCGCTCTTGACGAGAAATTCGCCGATGGC	1395
Qy	301	PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrTrpProTrpAsnIlePhe	320
Db	1396	TTTTGGCTAAGGGAGACAGCTGGTGTGTGGCAAGCAGACGACCCCTTGGAAATTTTC	1455
Qy	321	ProValIleSerLeuTyrLeuMetCysGluValThrAsnGlnSerPheArgIleThrIle	340
Db	1456	CCAGTCATTTCACTTACTCTCAAGGATGAAGTACCAACATAGCTCTTCGCGATACATC	1515
Qy	341	IleuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr	360
Db	1516	CTTCCTCAGCAATACCTACGGCGGGTGGAGGACGCGGCACTGCCCAAGACAGTGTAC	1575
Qy	361	LysPheAlaIleSerGlnSerSerThrCysIleValMetGlyAlaValIleMetGluGly	380
Db	1576	AAGTTCGCTGTCTCAAGCTCATCCACGGGCACTGTATTGGAGCGCGTCATCATGGAAGGT	1635
Qy	381	PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis	400
Db	1636	TTCTATGTGCGTCTTCGATCGAGCCCGAAAGCGAATTGGCTTGTGTGCAAGCTTGGCAT	1695
Qy	401	ValHisAspGluPheAspGlyThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu	420
Db	1696	GTGACGAGTAGGTTTCAGAGACGGCGCAGGTGGAAAGTCGTTTGTTCACGCAGACATGGAA	1755
Qy	421	AspCysGlyTyrAsnIleProGlnThrAspGlnSerThr	433
Db	1756	GACTGTGCTCAACATCTCCCAAGACAGTAGTCAACA	1794
RESULT 8			
AK046175			
LOCUS	4101 bp	mRNA	linear HTC 03-APR-2004
DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN		
VERSION	full-length enriched library, clone:BJ20346M13		
KEYWORDS	App cleaving enzyme, full insert sequence.		
SOURCE	AK046175.1 GI:26337868		
ORGANISM	AK046175		
REFERENCE	HTC; CAP trapper.		
AUTHORS	Mus musculus		
	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	Carniincl, P. and Hayashizaki, Y.		

TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	
AUTHORS	2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	
AUTHORS	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kitenaka, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iizawa, M., Ohara, E., Matsubiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiru, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	
AUTHORS	4
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
MEDLINE	Nature 409, 685-690 (2001)
PUBMED	5
REFERENCE	
AUTHORS	The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	6 (bases 1 to 410)
PUBMED	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kari, H., Kawai, J., Kojima, Y., Kondo, S., Komno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakakura, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
REFERENCE	
AUTHORS	Direct Submission
TITLE	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
JOURNAL	
MEDLINE	
PUBMED	
REFERENCE	
AUTHORS	
TITLE	cDNA library was prepared and sequenced in Mouse Genome Encyclopaedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
JOURNAL	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
MEDLINE	Please visit our web site for further details.
PUBMED	URL: http://genome.gsc.riken.jp/
REFERENCE	URL: http://Fantom.gsc.riken.jp/
AUTHORS	Location/Qualifiers
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AUTHORS	/db_xref="taxon:10090"
TITLE	/clone="B230346M13"

CDS

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AAITSDKPFINGSMWEGILGLVAIAIPDLSLEFSDLSKTHIPIFELQCA
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DKENYKDSIVDSTGTMRLPKVPEAAVKSIAASSPEKPDGFWIGBOLVCOAG
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ORIGIN

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 Pred. No.: 1,296-238 Length: 4101
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 Best Local Similarity: 96.30% Mismatches: 11
 Query Match: 96.63% Indels: 0
 DB: 3 Gaps: 0

US-10-726-967a-84 (1-433) x AK046175 (1-4101)

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QY 41 GluMetValAspAsnLeuArgGlyValSerGlyValGlyValTyrTyrValGluMetThrVal 60
DB 630 GAGATGCTGACAACTGAGGGGAAAGTCCGCGCAGGCTACTATGAGATGACCGTA 669
QY 61 GlySerProGluThrIleAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
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DB 1530 CTTCTCAACATTAACCTACGCGCGGTGAGGAGCTGGCCACGTCACCAAGACATGTTAC 1589
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DB 1650 TTCTATGCTGCTTGTGATGACCCGAAAGCAATTTGGCTTGTGCTGACGCTTGCCAT 1709
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DB 1770 GACTGTGCTACAACTTCCCAAGACAGATGATCAACA 1808

```

RESULT 9
 AK080498 3880 bp mRNA linear HTC 03-APR-2004
 LOCUS
 DEFINITION
 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:A73005X08 product:beta-site APP cleaving
 enzyme, full insert sequence.
 AK080498
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 (house mouse)
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99279253
 PUBMED
 10349636

REFERENCE
 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kondo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

MEDLINE
PUBMED
REFERENCE
AUTHORS
20499374
11042159
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komuro,H., Akiyama,J., Nishi,K., Kitanishi,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-Format
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE
JOURNAL
REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS
6 (bases 1 to 3880)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozumi,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komuro,H., Konda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohnato,N., Okazaki,Y., Saito,R., Saitoh,H., Sekai,C., Sekai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

TITLE
JOURNAL
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
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ORIGIN
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US-10-726-967a-84 (1-433) x AK080498 (1-3880)

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DB	635	CGATGTGGACAACTTGAGGGAAAGTCGGCCAGGAGCTATGTGGAGATGACCGTA	694
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DB	935	GCCATCACTGAATCGGCAAGATTCTTCATCAATGTTCCAATCGGAGGCGATCCAGGG	994
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DB	995	CTGGCTATGCTGATGATGGCAGGCCGAGCATCTTTGAGGCCCTTTGACTCCCTG	1054
QY	181	Vallyseglnthr1bvalProaenleupheserleuglnleucygl1alaglyphep	200
DB	1055	GTGAAGCAGACCCACATTCACATCTTTCCCTCAGCTGTGGCGCTGCCCTCCCC	1114
QY	201	Leuasn1sergluValleuAlaSerValGlySerMet1le1le1lyl1leap	220
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QY	221	H1serleuTyThrGlySerleuTyTyThrPro1leargrsglulTyTyTyglu	240
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QY	241	Val1le1le1ValargyValglulleanglygl1asnpleu1yweacapylysglyTy	260
DB	1235	GTGATCATTTGTATGTTGTGGAAATCAATGTGTCAAGATCTCAAGATGACGCAAGGAGTAC	1294
QY	261	AsnTyraaplyser1leValaapserglTyThrAsnleuargleuProlyllybVal	280
DB	1295	AACTCAGCAAGGACCTTTGTGACATGTGGACCAACCACTTCGCTGCCAAGAAAGTA	1354
QY	281	PheglualalalVallyser1le1yba1a1aserSerThrGlyllysrPheProapgl	300
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QY	301	PheTTPleuglygluglnleuValCyrtPgl1na1aglyTyThrProTPraen1lepe	320
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 RESULT 10 3805 bp mRNA 1linear HTC 03-APR-2004
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 LOCUS AK082230
 DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone: C230026008 product: beta-site APP cleaving
 enzyme, full insert sequence.
 ACCESSION AK082230.1 GI:26100512
 VERSION AK082230.1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahwagi, K.,
 Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system -384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE
 AUTHORS The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 3805)
 JOURNAL
 REFERENCE
 AUTHORS
 1 ThnGlnHisGly11leArgLeuProLeuAspGlyLeuGlyValAlaProLeuGlyLeu 20
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 DB 571 AGGCTGCCCGGAGACGACGAGGAAATCGAGAGCTTGGCCGCGAGGCGAGCTTGTG 630
 QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyTyrValGluMetThrVal 60
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 QY 61 GlySerProGln1ThyLeuAsn1leLeuValAspThyGlySerSerAsnPheAlaVal 80
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 Score: 2181.00 Matches: 417
 Percent Similarity: 97.01% Conservatve: 5
 Best Local Similarity: 95.86% Mismatches: 11
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 1 ThnGlnHisGly11leArgLeuProLeuAspGlyLeuGlyValAlaProLeuGlyLeu 20
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 QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyTyrValGluMetThrVal 60
 DB 631 GAGATGTGTGACCACTGAGGGGAAAGTCCGGCGAGGCTACTATGTGAGATGACCGTA 690
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 DB 871 GGGGACCGACCTGTGTAGCATCCCTCATGGCCCCAAGCATGCTGGGTCCCAACATTGC 930
 QY 140 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTrpGluGlyIleLeuG 160
 DB 931 TGCCTACTGTAATCGACAAAGTCTTCAATAGTTCACACTGGAGGGGCATCTCTAGG 990
 QY 160 YLeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSer 180
 DB 991 GCTGGCCTATGTGAGATTGCCAGGCCGACGACTCTTGGAGCCCTCTTTCATCTCCCT 1050
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 DB 1051 GGTGAAGCAGACCCACATTCCTCCAAACATCTTTCCTGCAGCTCTGTGGCGCTGCC 1110
 QY 200 oLeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyIleLeu 220
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 QY 240 UValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysGlyGlu 260
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 QY 260 rAsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysLeu 280
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 QY 280 lPheGluAlaAlaValLysSerIleLysAlaAlaSerSerThrGluLysPheProAsp 300
 DB 1351 ATTTGAAGCTGCGCTCAAGTCCATCAAGGACAGCTCTCTCGACGAGAACTCCCGA 1410
 QY 300 yPheTrp-LeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIle 320
 DB 1411 CTTTGGGCTAGGGAGAGAGCTGTGTCTGGCAAGGAGCGACGACCCCTTGGAACTTT 1470
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 DB 1471 TCCCAAGTCAATTCATCTTACTCATGGGTGAAGTACCAATCATGCTTCCGATACCA 1530
 QY 340 lLeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCys 360
 DB 1531 TCTTCTCTAGCAAAATCCTACGCGGGTGAAGAGAGTGGCCAGTCCCAAGACGACTTT 1590
 QY 360 yLysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyValAlaIleMetGlu 380
 DB 1591 ACAAGTGGCTGTCTCACAGTATCCAGGGGACGCTTATGGGAGCCCTCATCATGAG 1650
 QY 380 lYpHeTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCys 400
 DB 1651 GTTTCATGTGCTCTCTTCATTCAGGCCGCAAGCGAAATGGCTTGTCTGACGCGTTC 1710
 QY 400 lValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMet 420
 DB 1711 ATGTGACGATAGATTCCAGAGGCGGCGAGTGGAAAGTCCGTTGTGTACGGCAGACAT 1770
 QY 420 lAspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
 DB 1771 AAGACTGTGGCTACAACTTCCCGACAGACATGAGTCAACA 1811

RESULT 11

AK082317
LOCUS
DEFINITION

AK082317
4048 bp mRNA linear HTC 03-APR-2004
Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
enriched library, clone: C230037E16 product: beta-site APP cleaving
enzyme, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK082317.1 GI:26349644
AK082317.1
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS
JOURNAL
MEDLINE
PIRME

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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REFERENCE

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL
MEDLINE
PIRME
REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitesuna, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashinaga, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuyama, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

TITLE

THE RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

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FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

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AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

TITLE

5 (bases 1 to 4048)
Adachi, U., Aizawa, K., Akiyama, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohnato, N.,
Ohtsuka, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akihara, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

REFERENCE

Submitted (16-APR-2002) Yoshinori Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suhei-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.jp,
URL: http://genome.resgsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

TITLE

CDNA library was prepared and sequenced in Mouse Genome

JOURNAL

CDNA library was prepared and sequenced in Mouse Genome

COMMENT

CDNA library was prepared and sequenced in Mouse Genome

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 Mukayoyca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
2 Carninci, P. and Hayashizaki, Y.
3 High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
2 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20493374
11042159

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komono, H., Akiyama, J., Nishi, K., Kitsuai, T., Taahito, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Futsuke, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.
2 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
2 Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
2 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3147)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

1 Adachi, J., Aizawa, K., Akimura, T., Aikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komono, H., Kusakawa, M., Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takenashi, F., Takaku-Akahira, S., Tagada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
2 Direct Submission
Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sueno-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-research.riken.jp, fax:81-45-503-9216]
URL: <http://genome.gsc.riken.jp/>, Tel.81-45-503-9222

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
Location/Qualifiers
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DEFINITION		IMAGE:6585124 5', mRNA sequence.		
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VERSION		BUS57282.1 GI:22907578		
KEYWORDS		EST.		
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		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE		1 (bases 1 to 928)		
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/.		
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D. Email: rgs@bbs-rcmail.nhl.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LINC2796 row: j column: 04 High quality sequence start: 28 High quality sequence stop: 688. Location/Qualifiers		
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ORIGIN	NTF_MGC Library."			
Alignment Scores:	1.83e-150	Length:	928	
Pred. No.:	1425.00	Matches:	285	
Percent Similarity:	95.99%	Conservative:	2	
Best Local Similarity:	95.32%	Mismatches:	6	
Query Match:	62.28%	Indels:	5	
DB:	5	Gaps:	2	
US-10-726-967A-84 (1-433) x BUS57282 (1-9248)				
QY	131	ProAsnValThrValArgHisAsnIleAlaIleThrGluSerAspLysPhePheIle	150	
DB	36	CCCAAGCTACCTGTGGGTCCAACATTCCTGCATCACTGATACAGACAGTCTTTCATC	95	
QY	151	AsnGI SerAsnTrpGluIylIleLeuGIyleuAlaTralacIuIleAlaIarPProAsp	170	
DB	96	AACGGCTCCAACTGGGAAGGATCCTGGGGGCTGGCTATGCTGAGATTGCCAGGCTGAC	155	
QY	171	AspSerLeuGluIuProPhePheAspSerLeuValLysGIinThrHisValProAsnLeuPhe	190	
DB	156	GACCTCCCTGGAGCTTTCTTTGACTCTCGTAAGAGCAGACCCAGTCCCAACCTTTC	215	
QY	191	SerLeuGluIuLeuCyseGIylalacIylPheProLeuLanGIinSerGIuValLeuAlaSerVal	210	
DB	216	TCCCTGAGCTGTGTGTGTCTGGCTTCCCTCCCAACAGCTGAGAGCTGTGGCTGTGC	275	
QY	211	GIyGIySerMetIleIleGIyGIyIleAspHisSerLeuTrpThrGIySerLeuTrpTrp	230	
DB	276	GGAGGAGCATGATCTTTGGAGGTATCAACACTGGCTGTACAGGCAAGCTCTGGTAT	333	
QY	231	ThrProIleArgTrsGluTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp	255	
DB	336	ACACCCATCCGGGGAGGTGATTATAGGTCATCATTTGGCGGGTGGAGATCAATGGA	395	
QY	251	GlnAspLeuLysMetAspCysIyGIuTrpAsnTrpAspLysSerIleValAspSerGIy	270	
DB	396	CAGATCTGAAATGAGCTGCAAGAGATCAACTGTGCAAGAGATTTGGAGACAGTGGC	455	
QY	271	ThrThrAsnLeuArgLeuProLysValPheGluAlaIleValLysSerIleLysAla	290	
DB	456	ACACCAACCTTGTGTGCCCAAGAAAGTGTGAAAGCTGACGTCAATCACTCAAGCA	515	
QY	291	AlaSerSerThrGluLysPheProAspGIyPheTrpLeuGIyGluGluLeuValCysTrp	310	
DB	516	GCCTCCCTCCAGGAAAGTTCCCTGATGTTCTGGTATGAGAGACAGCTGTGTGTGG	575	
QY	311	GlnAlaGIyThrThrProTrpAsnIlePheProValIleSerLeuTrpLeuMetGIyGlu	330	
DB	576	CAAGCAGGCAACCCCTTGAAACATTTCCAGAGCATCTCACTTACTTATGGGTGAG	635	
QY	331	ValThrAsnGlnSerPheArgIleThrIleLeuProGlnGIyTrpLeuArgProValGlu	350	
DB	636	GTTACCAACAGCTTCCGATCAACATCTTCCGACCAATACCTCCGCGCAGTGGAA	695	
QY	351	AspValAlaThrSerGlnAspAspCysTrpLysPheAlaIleSerGlnSerSerThrGIy	370	
DB	696	GATGTGGCCACGTCCCAAGACAGCTTCAAGATTGGCATCTCACTCACTCCAGGGC	755	
QY	371	ThrValMetGIyAlaValIleMetGIyGIyPheTrpValValPheAspArgAla-Argly	390	
DB	756	ACTGTATGGACCTGTATCACTGAGGGCTTCACTGTGTCTTGTGATCGGGCCCGAAA	815	
QY	390	ArgIle-GlyPheAlaVal-SerAlaCysHisValHisAspGluPheArgThrAlaAla	405	
DB	816	ACGATTGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	875	
QY	410	---ValGIuGIyPro-PheValThrLeu---AspMetGluAspCysGIy 423		
DB	876	CGGTGAAAGGCCCTTTTGTCTACCTTGGAAACATGGGAAAGCTGTGG 924		

RESULT 14
BU128383 1001 bp mRNA linear EST 25-NOV-2002
LOCUS 603113984F1 CSECHL20 Gallus gallus cDNA clone CHEST65g21 5', mRNA
DEFINITION
ACCESSION BU128383
VERSION BU128383.1 GI:25339782
KEYWORDS
SOURCE EST
ORGANISM Gallus gallus (chicken)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE
1 (bases 1 to 1001)
Boatman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNA
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
MEDLINE
PUBMED 12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
Location/Qualifiers
1..1001
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CHEST65g21"
/dev_stage="36"
/lab_host="DH10B"
/note="Organ: 1limb; Vector: pBluescript II KS(+); Site 1:
EcoRI, Site 2: NotI; Modification of Bluescript II KS(+)
(Stratagene) vector to accommodate cDNA produced with the
1-stranded protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
ligate in double stranded adaptor containing BamI and
BamH sites (5'gaccgcgcagcccgatccgaaataag)
(5'aattcttttcggatccg99gctgcagc)"
ALIGNMENT SCORES:
Pred. No.: 8 51e-145 Length: 1001
Score: 1375.50 Matches: 287
Percent Similarity: 89.61% Conservative: 15
Best Local Similarity: 85.16% Mismatches: 32
Query Match: 60.12% Indels: 8
DB: 5 Gaps: 0
US-10-726-967a-84 (1-433) x BU128383 (1-1001)
QY 55 TyrValGluMetThrValGlySerProProGlnThrLeuAsnIleLeuValAspThrGly 74
DB 2 TACGTGAGATGACGCTGGGACGCCCGCGAGAGCTCAATATCTGCTGGAGACTGGG 61
QY 75 SerSerAspMetIleValGlyAlaIleProHisProPheLeuHisArgTyrTyrGlnArg 94
DB 62 AGCAATTAATTTGGCTGTGGAGCTGCACCTCACTTCTCCGAGATACTACACGCGG 121
QY 95 GlnLeuSerSerThrTyrArgAspLeuArgGlyGlyValTyrValProTyrThrGlnGly 114
DB 122 CAGCTGTCAAGACTTACCTGACCTGGCGGAAGGGTGTGTATGTGCTTACACCA-GGC 180
QY 115 LysTrpGlnGlyGluLeuGlyThrAspLeuValSerIleProHisGlyProAsnValThr 134

DB 161 AAGTGGAGAGGAGGCTGGGACCTGACCTTGTCCACTCCCTCCCGCCCAAGCTGACT 240
QY 135 ValArgAlaAsnIleAlaIleThrGluSerAspPhePheIleAsnGlySerAsn 154
DB 241 GTCAAGCCCAATCTGCTGCATCAAGAGTCACACAAATTTCTTCAATCATGCTCCAC 300
QY 155 TrpGlnGlyIleLeuGlyLeuValTyrAlaGlnIleAlaArgProAspAspSerLeuGlu 174
DB 301 TGGGAAGGAGATCTGGGCTGGCTGCTAGTATCCACAGCGCTGCACAGACGCTGAG 360
QY 175 ProPhePheAspSerLeuValGlyThrHisValProLeuLeuPheSerLeuGlnLeu 194
DB 361 CCTTTTGTATCTCTGGTGAACACACCCAGGTGGCCCAACATCTTCTCTCCACTT 420
QY 195 CysGlyAlaGlyPheProLeuAsnGlnSerGlyValIleuAlaSerValGlyGlySerMet 214
DB 421 TGTGGGGCAGGCTTCTACCCCAAGACAGACAGACTTGGCATCAGTGGAGGAGCATG 480
QY 215 IleIleGlyGlyIleAspHisSerLeuTyrThrGlySerLeuTyrThrProIleArg 234
DB 481 ATCATTTGTGCATCGACCGCTCGCTGTATGTGGTGATCTGTGTACACACCATCCGG 540
QY 235 ArgGluTrpTyrTyrGluValIleIleValArgValGluIleAsnGlyIleAspLeuLys 254
DB 541 AAGAGTGTGATCTACGAGGTGATCATTTGTCAAGCTGAGGTCAATGGGACGCTGAC 600
QY 255 MetAspCysIleGlyTyrAsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeu 274
DB 601 ATGACTGTCAAAAGATCAACTATGACACAGATATCGTGACAGTGGCACCAACCTC 660
QY 275 ArgLeuProIleLysValIleGluAlaIleValIleSerIleLysValAlaIleSerThr 294
DB 661 AGGCTGCCGAAGAGGGTGT-GAGGCCGACGTAAATCAATCAAAACAGCTTCTTGACA 719
QY 295 GlnLysPheProAspGlyPheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThr 314
DB 720 GAGAAATGCCCAATGGCTCTTGTGGTGGGAGACAGCTGTTTGTGGCAGGTCCGACCA 779
QY 315 ThrProTrpAsnIlePheProValIleSerLeuTyrLeuMetGlyGluValThrAsnGln 334
DB 780 C--CCCTGGGACATCTTCCCTGTTCTGCTCCTTACTGATGGGGAGGCGCAC-AAACAG 836
QY 335 SerPheArgIleThrIleLeuProGlnGlnTyrLeuArgProValGluAspValAlaThr 354
DB 837 TCTTCCGATTCACATCTTCTCCAGCAATACCTGGGCCAGTGAAGAACTGTGGCCACT 896
QY 355 SerGlnAspAsp-Cys-TyrLysPheAlaIleSerGlnSerSer-ThrGlyThrValMet 373
DB 897 CTCAGGATGACCTGCTCCTACAGGTTGACAACTCTCAGGCTCTCCACAGCAGCTCATG 956
QY 374 GlyAlaValIleMetGlnGlyPheTyrValValPheAspArgAla 388
DB 957 GGGTGTGTATCCAGAGGGGTCCACCTGGC-TTTGACCGGGGCC 1000
RESULT 15
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LOCUS AGENCOURT_10023278 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5481022
DEFINITION
ACCESSION BU502697
VERSION BU502697.1 GI:22807818
KEYWORDS
SOURCE EST
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 950)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.llnl.gov
 Plate: L1CM2661 row: 1 column: 15
 High quality sequence stop: 620.
 Location/Qualifiers

FEATURES

1..950
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6481022"
 /tissue_type="carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_40"
 /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 King Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,22e-143 Length: 950
 Score: 1365.00 Matches: 277
 Percent Similarity: 94.59% Conservative: 3
 Best Local Similarity: 93.58% Mismatches: 10
 Query Match: 59.66% Indels: 7
 DB: 5 Gaps: 2

US-10-726-967a-84 (1-433) x BU502697 (1-950)

QY 58 MetThrValAlaGlySerProPheGlnThrLeuAsnIleLeuValAspThrGlySerSerAsn 77
 DB 1 ATGACCGTGGGCGAGCCCCCGGAGAGCGTCAACATCTGTGGATACAGGAGCACTAAC 60
 QY 78 PheAlaValAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSer 97
 DB 61 TTGGCAGTGGGTGCTGCCCCCCTCTGCTGCTACTACCAAGGAGGAGCTGTGCC 120
 QY 98 SerThrTyrArgAspLeuArgLysGlyValTyrValProTyrThrGlnGlyLysTrpGlu 117
 DB 121 ACCACATACCGGAGCCTCCGAGAGGTGTGTATGTCCTCAACCCAGGAGCAAGTGGAA 180
 QY 118 GlyGluLeuGlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAla 137
 DB 181 GGGAGACTGGGCGACCACTGGTACATCCCAATGAGCCCACTGAGCTGTGCC 240
 QY 138 AsnIleAlaAlaIleThrGlnSerAspLysPhePheIleAsnGlySerAsnTrpGluGly 157
 DB 241 AACATTGCTGGCCATCACTGAATCAGACAAAGTCTTCATCAACGGCTCAACTGGAAAGGC 300
 QY 158 IleLeuGlyLeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePhe 177
 DB 301 ATCCCTGGGGCTGGCTATGCTGAGATTGCCAGGCTGACACTCCCTGGAGCCTTCTTT 360
 QY 178 AspSerLeuValLysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCyseGlyAla 197
 DB 361 GACTCTCTGTAAAGCAAGCAACGTTCCCAACTCTTCTCCCTGCAAGCTTTGGAGCT 420
 QY 198 GlyPheProLeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGly 217
 DB 421 GGCTTCCCTCAACGAGTGTGAAGTGTGGCTCTGTCCGAGGAGCATGATCATTTGGA 480
 QY 218 GlyIleAspHisSerLeuTyrThrGlnLysSerLeuTrpTyrThrProIleArgArgGluTrp 237
 DB 481 GGATGACCACTCGCTGACAGGAGGCTCTCTGGATACCCCAATCCGGCGGAGTGG 540

QY 238 TyrTyrGluValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCys 257
 DB 541 TATTATGAGGTGATCATTTGTGGGTGAGATCAATGACAGATCTGAAAAATGACTGC 600
 QY 258 LysGluTyrAsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuPro 277
 DB 601 AAGGATACAACTATGACCAAGCATTTGTGACAGTGGCAACCAACTTCGTTTGCC 660
 QY 278 LysLysVal-PheGluAlaAlaValLysSerIleLysAlaSerSerThrGluLysPhe 297
 DB 661 AAGAAAGTGTTCAGAGCTGACGTCAAATTCATCAAGGAGCACTCTCCAC-GAGGAGTT 719
 QY 297 eProAspGlyPheThrLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTr 317
 DB 720 CCTGATGTTCTGGCTAGAGAGACACTGTGTGTGCTGGCAAGCAGGACACCCCTTG 779
 QY 317 PAsnIlePhe-ProValIleSerLeuTyrLeuMetGly---GluValThrAsnGln-Ser 335
 DB 780 GAACATTTTCCCACTCATCTCACTCACTCAAGGGGTAGAGTTACCAACCAAGTCC 839
 QY 336 Phe-ArgIleThrIleLeuProGln---GlnTyrLeuArg 347
 DB 840 TTCCGATCAACATCCCTCCCGCAGCAATTAACCTGCGG 879

Search completed: August 22, 2005, 05:04:19
 Job time : 5810 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 21, 2005, 09:05:38 ; Search time 59 Seconds
(without alignments)
706.133 Million cell updates/sec

Title: US-10-726-967a-84

Perfect score: 2268
Sequence: 1 TQHGIRLPRLRSGLGAPLGL.....FTVLDMEDCGYNIPQTEST 433

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2267	99.1	501	2 A59090	aspartic proteinase
2	311	13.6	384	2 JC7574	pepsinogen A - Afr
3	311	13.6	387	2 B38302	pepsin (EC 3.4.23.
4	308	13.5	385	2 JC7575	pepsinogen A - bul
5	304.5	13.3	383	2 JC7573	pepsinogen C - Afr
6	302.5	13.2	388	1 S19682	pepsin A (EC 3.4.2
7	302	13.2	384	2 A39314	gastricsin (EC 3.4
8	301	13.2	382	1 PECH	pepsin A (EC 3.4.2
9	299.5	13.1	396	2 A34401	cathepsin E (EC 3.
10	298.5	13.0	383	2 A41443	pepsin (EC 3.4.23.
11	296	12.9	387	2 C38302	cathepsin B (EC 3.
12	296	12.9	391	2 A43356	cathepsin D (EC 3.
13	296	12.9	407	1 KHRD	cathepsin D (EC 3.
14	295.5	12.9	412	1 KHRD	pepsin (EC 3.4.23.
15	295	12.9	387	2 D38302	pepsin A (EC 3.4.2
16	289.5	12.7	388	1 S19684	cathepsin D (EC 3.
17	287.5	12.6	410	1 T24204	hypothetical prote
18	287.5	12.6	444	1 T24204	pepsin (EC 3.4.23.
19	286	12.5	387	2 E38302	cathepsin B (EC 3.
20	285.5	12.5	398	2 S66465	chymosin (EC 3.4.2
21	285	12.5	380	2 I47176	chymosin D (EC 3.
22	285	12.5	388	1 I51185	cathepsin D (EC 3.
23	283.5	12.4	388	1 PEMQAR	pepsin A (EC 3.4.2
24	282.5	12.3	389	1 PEMQAR	pepsin A (EC 3.4.2
25	282	12.3	389	1 JE0371	pepsin C (EC 3.4.2
26	281.5	12.3	381	1 CMSHB	chymosin (EC 3.4.2
27	281.5	12.3	388	1 PEMQAR	pepsin A (EC 3.4.2
28	281.5	12.3	388	2 A30142	pepsin A (EC 3.4.2
29	279.5	12.2	388	2 B30142	pepsin A (EC 3.4.2

30	278.5	12.2	386	1 PEPC	pepsin A (EC 3.4.2
31	278	12.2	387	2 JC7245	pepsinogen A - com
32	277.5	12.0	396	2 S36865	cathepsin E (EC 3.
33	273.5	12.0	381	1 CMBO	chymosin (EC 3.4.2
34	270.5	11.8	377	1 PEMQCC	gastricsin (EC 3.4
35	270.5	11.8	389	2 A38302	pepsin (EC 3.4.23.
36	270	11.8	376	2 I45856	aspartic proteinase
37	268.5	11.7	344	1 KHRPD	cathepsin D (EC 3.
38	267.5	11.7	381	2 JC7247	prochymosin (EC
39	267	11.7	380	2 S03433	candidapepsin (EC
40	266	11.6	405	2 A25379	baaccharopepsin (EC
41	265.5	11.6	396	2 T47207	aspartic proteinase
42	263.5	11.5	388	2 JC7246	pepsinogen C - com
43	262.5	11.5	394	2 B43356	gastricsin (EC 3.4
44	261.5	11.4	387	2 A45117	aspartic proteinase
45	261.5	11.4	388	2 A29937	gastricsin (EC 3.4

ALIGNMENTS

RESULT 1
A59090
aspartic proteinase (EC 3.4.23.-) BACE precursor - human
N.Alternate names: beta-secretase; beta-site APP cleaving enzyme
C.Species: Homo sapiens (man)
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C.Accession: A59090
R.Vassar, R.; Bennett, B.D.; Babu-Khan, S.; Kahn, S.; Mendiaz, E.A.; Denis, P.; Teplow, M.A.; Biero, A.L.; Curran, E.; Burgess, T.; Louis, J.C.; Collins, F.; Tseanor, J.; Rogers
A>Title: beta-Secretase cleavage of Alzheimer's amyloid precursor protein by the transmembrane
A.Reference number: A59090; PMID:20002972; PMID:10531052
A.Note: submitted to GenBank, September 1999
A.Accession: A59090
A.Status: not compared with conceptual translation
A.Molecule type: mRNA
A.Residues: 1-501 <VAS>
A.Cross-references: UNIPROT:P56817; GB:AF190725; NID:g6118538; PIDD:AAF04142.1; PID:g611
C:Gene: BACE
C:Superfamily: beta-secretase
C:Keywords: Alzheimer's disease; aspartic proteinase; brain; glycoprotein; hydrolase; pr
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-45/Domain: propeptide #status predicted <PRO>
F:46-501/Product: acid proteinase BACE #status predicted <MAT>
F:461-477/Domain: transmembrane #status predicted <TRN>
F:93-289/Active site: Asp #status predicted
F:153-172,223,354/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:330-380/Disulfide bonds: #status predicted

Query Match
Best Local Similarity 99.1%; Score 2267; DB 2; Length 501;
Matches 429; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY	1	TQHGIRLPRLRSGLGAPLGLRLPRETDEPEERGRSGVENVNLRGSGGGYVEMV	60
DB	22	TQHGIRLPRLRSGLGAPLGLRLPRETDEPEERGRSGVENVNLRGSGGGYVEMV	81
QY	61	GSPPTLNTLVYTGSSNFAVGAAPPFLRRYQROLSTYRDLRKGVVYPYQKWEGL	120
DB	82	GSPPTLNTLVYTGSSNFAVGAAPPFLRRYQROLSTYRDLRKGVVYPYQKWEGL	141
QY	121	GTDLVSIPIHGPVYVYRANIAITSDKPFINSNMEGIGLAVAIARPDSDLPEPFDL	180
DB	142	GTDLVSIPIHGPVYVYRANIAITSDKPFINSNMEGIGLAVAIARPDSDLPEPFDL	201
QY	181	VQOTHPVNFSLQLCAGGAPLQSVLASVGSMTIGIGDHSGLYGSIMTYTIRRWYR	240
DB	202	VQOTHPVNFSLQLCAGGAPLQSVLASVGSMTIGIGDHSGLYGSIMTYTIRRWYR	261
QY	241	VIVRVEINGDGLKMDCKEYNDKSIYDGTNLRPKVVFPAAVKSIKAASTKFPDG	300
DB	261	VIVRVEINGDGLKMDCKEYNDKSIYDGTNLRPKVVFPAAVKSIKAASTKFPDG	321

Db 262 VTIIVVEINGODLKMDCKEVNDKSIYDSGTTNLRPKVEEAAVKSIAKSTKEPDG 321
QY 301 FVLGEOLVCMQAGTTPNANIFPVISLYLMGEVTVNSFRITLIPQOYLKRPVEDVATSDDDCY 360
Db 322 FVLGEOLVCMQAGTTPNANIFPVISLYLMGEVTVNSFRITLIPQOYLKRPVEDVATSDDDCY 381
QY 361 KPAISQSTGTVMKAVIMEGFYVYVDRARRKIGFAVSAACHVHDEFRTAAVEGPFVTLDM 420
Db 382 KPAISQSTGTVMKAVIMEGFYVYVDRARRKIGFAVSAACHVHDEFRTAAVEGPFVTLDM 441
QY 421 DCGYNIPQTDST 433
Db 442 DCGYNIPQTDST 454

RESULT 2

pepsinogen A - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07574, PC7119
R/Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasa, S.
J. Biochem. 129, 147-153, 2001
A/Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A/Reference number: J07573; MUID:21064922; PMID:11134969
A/Contents: Stomach
A/Accession: J07574
A/Molecule type: mRNA
A/Residues: 1-384 <IKU>
A/Cross-references: UNIPROT:Q9DEC2; DDBJ:AB045380
A/Accession: PC7119
A/Molecule type: Protein
A/Residues: 16-35;57-76 <IK2>
C/Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like
C/Genetics:
A/Gene: P9A
C/Superfamily: pepsin
C/Keywords: stomach; zymogen

Query Match 13.6%; Score 311; DB 2; Length 384;
Best Local Similarity 25.1%; Pred. No. 2e-17;

Matches 107; Conservative 69; Mismatches 154; Indels 96; Gaps 18;

QY 5 IRLPLRSLGAGPLGLEINLETDDEPEERGRGSFVE-----MVDNLR 47
Db 17 VKVPLRK-----ESFRNRQRGLGLDYLKKVPNPAKVPPTLAQSAETLQ 65
QY 48 GKSQGGYVEMTVGSPQTLNLTVDTSNFAVGAAPHFL-----HRYQRQLSSTY 100
Db 66 NYMDLEYGTISIGTPQEFVIFDTSANLWV---PSYCSSQACSNHNFNPQSSSTF 122
QY 101 RDLRKGVVYVYQKKEGELGTDLSVPHGPVTVRANAAITTESDK-FPINGSWBEIL 159
Db 123 QATNTPVSIQYGTGMSGLGYDTLQV--GNIQISNQMFGLSSEPSGLYSPFDGL 179
QY 160 GLAYELIARPDLSLEPFDSLQKTHVP-NFSLQLCGAGPLNQSEVLASVGSMTIG 218
Db 180 GLAFPSIA--SSQATPVFEDNMWSQGLIPNLFSLVLSDD-----QTGSVYLF 227
QY 219 IDHSLYTGSGLWYTPIRREYVYVILVVEINGODL--KMDCKEYVDKSIYDSGTTNLR 276
Db 228 VDNSTYSSGLNKNVPLTAETITWITLDSVINGQVYACQSC--QATVDGTSMTG 281
QY 277 PKRVEAAVKSIAKSTKEPDGFWLGEOLV-CMQAGTTPNANIFPVISLYLMGEVTVNS 335
Db 282 PSTPI-ANIQVYIGASQDSN-----GQYVINCNNISNMTIYF----- 318
QY 336 FRITLIPQOYLKRPVEDVATSDDDCY-KAISQSTGT---VNGAVIMEGFYVDRAR 389
Db 319 ---TINGVQYPLSPAVYVRONQCGSSGFGQAMNLPNMSGDLMTIGDVFIHQYFTVDRAN 375
QY 390 KRIGFA 395

Db 376 NYVALA 381

RESULT 3

pepsin (BC 3.4.23.-) II-1 precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 14-Jun-1991 #sequence_revision 20-Sep-1991 #text_change 16-Aug-2004
C/Accession: B38302
R/Kagiyama, T.; Tanabe, K.; Koizumi, O.
J. Biol. Chem. 265, 17031-17038, 1990
A/Title: Structure and development of rabbit pepsinogens. Stage-specific zymogens, nucle
A/Reference number: A38302; MUID:91009127; PMID:2129536
A/Accession: B38302
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-387 <KAG>
A/Cross-references: UNIPROT:P28712; GB:M59235; GB:J05638
C/Superfamily: Pepsin
C/Keywords: aspartic proteinase; hydrolase; phosphoprotein; protein digestion

Query Match 13.6%; Score 311; DB 2; Length 387;
Best Local Similarity 26.6%; Pred. No. 2e-17;

Matches 105; Conservative 72; Mismatches 145; Indels 72; Gaps 17;

QY 23 NLETDDEPEERGRGSFVEM-VNLRKSGSGQYVEMTVGSPQTLNLTVDTSNFAVG 81
Db 48 NLATKYPK-----TFASVSTESLENYLDAEYFGTISICTPQEFVIFDTSNLMWP 102
QY 82 ----AAHPLRLRYQRQLSSTYRDLKGVYVYVYQKKEGELGTDLSVPHGPVTVRA 137
Db 103 STYCSLACFLHRRFNDSDSTFOATSETLSTYVGSMTGILGYDTVAV--GNIEDTN 159
QY 138 NIAAITESD---KFPINGSWEGILGLAYELIARPDLSLEPFDSLQKTHV-PNIFSLQ 193
Db 160 QIFELSKTEBGTITFLV-APFDGILGLAIPSAISASAT--PVFDNMNGLVSEDFSY 215
QY 194 LCGAGPLNQSEVLASVGSMTIGIDHSLYTGSGLWYTPIRREYVYVILVVEINGODL 253
Db 216 LSSNG-----BKGSVMFGGIDSSYVTSNLMWVPSHEGWQVIMDSITINGERTI 265
QY 254 KM--DCKEYVVDKSIYDSGTTNLRPKKVEEAAVKSIAKSTKEPDGFWLGEOLV-CW 310
Db 266 ACADSC-----QAVDTGSLAGPTSAISKIYSTIGASKUL-----LGENIISCS 311
QY 311 QAGTTPNANIFPVISLYLMGEVTVNSFRITLIPQOYLKRPVED-VATSDDC--YKFAISQ 366
Db 312 AIDSLPDIYF-----TINNVQPLPASAVILKEDDDCLSGFGQAMLD 353
QY 367 SSTGT--VNGAVIMEGFYVDRARRKIGFAVSA 398
Db 354 TSYGELMTIGDVFIHQYFTVDRANQVGLAAA 387

RESULT 4

pepsinogen A - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C/Accession: J07575
R/Ikuzawa, M.; Inokuchi, T.; Kobayashi, K.; Yasumasa, S.
J. Biochem. 129, 147-153, 2001
A/Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A/Reference number: J07573; MUID:21064922; PMID:11134969
A/Contents: Stomach
A/Accession: J07575
A/Molecule type: mRNA
A/Residues: 1-385 <IKU>
A/Cross-references: UNIPROT:Q9DEC4; DDBJ:AB045376
C/Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like
C/Genetics:
A/Gene: P9A
C/Superfamily: pepsin

C:Keywords: stomach; zymogen

Query Match 13.5%; Score 308; DB 2; Length 385;
Best Local Similarity 27.8%; Pred. No. 3.5e-17;
Matches 99; Conservative 64; Mismatches 133; Indels 60; Gaps 15;

QY 54 YVENVTVSGPPTLNIIVDTGSSNFAVG---AAHPFLHRYRQQLSTYDIAKGVV 109
DB 73 YFGTISIGTPQSFVYIPDTGSSNLMWPSVSCSPACTNHMFNPQOSTFQATNTPVSI 132
QY 110 PTTQKMEGELGTDVSIHGPNTVFRANIAITAESDK-FPINGSNMEGILGLAYAEIAR 168
DB 133 QGTGSMGSGFLGIDYVQV---GNIQITNQIFGLSGSEPSFLYSPFGDILGLAFPSLA- 188
QY 169 PDDSLPEPFDLSVKQTHVP-NLPSLQLCAGFPLNQSEVLASVGSMTIIGIDHSLYTG 227
DB 169 -SSQATPVPDMMNQGLIQDLPFSVYLSGQ---QS-----GSFVLFGVDTSYTCN 237
QY 228 LMYTPIRREMYEVIIVVEINGDLKM--DCKENYDKSIYDSGTTNLRPKVFEAAV 285
DB 238 LNWVPLTAEYVQITVDSISIGQVYACSGC-----SAIVDTGTSLAGP-----STPI 287
QY 286 KSIAKASSTKPPDGMGLGEOLVCMQAGTTPMNIPEVISLYLMGEVTSQSPRITILPOQY 345
DB 288 ANIQYITGANQDSNGQYV---INCNNISMPYVVF-----TINGVQY 326
QY 346 LRPVDD-VATSDDDC---YKPAISQSTGT--VMGAVIMEGYVVFDRARKIGFA 395
DB 327 PLPAAVYRQSQSCSGSQANLPLPSSDLMILGQVFRREYVYVDRANNVYAMA 382

RESULT 5

JC7573
pepsinogen C - African clawed frog
N.Alternate names: progastricin
C.Species: Xenopus laevis (African clawed frog)
C.Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C.Accession: JC7573; PC7118
R.Ikuwawa, M.; Inokuchi, T.; Kobayashi, K.; Yasunasu, S.
J. Biochem. 129, 147-153, 2001
A.Title: Amphibian pepsinogens: Purification and characterization of Xenopus pepsinogens
A.Reference number: JC7573; MUID:21064922; PMID:11134969
A:Contents: Stomach
A:Accession: JC7573
A:Molecule type: mRNA
A:Residues: 1-383 <IKU>
A:Cross-references: UNIPROT:Q9DEB3; DDBJ:AB045379
A:Accession: PC7118
A:Molecule type: protein
A:Residues: 17-68 <IK2>
C.Comment: This protein is a zymogen for gastric aspartic proteinase, with pepsin-like A
C.Genetic: PGC
A:Gene: PGC
C:Superfamily: pepsin
C:Keywords: stomach; zymogen

Query Match 13.3%; Score 304.5; DB 2; Length 383;
Best Local Similarity 26.0%; Pred. No. 6.8e-17;
Matches 112; Conservative 64; Mismatches 140; Indels 115; Gaps 19;

QY 2 OHGIRLPLRSGLGAGAPLGLINLETDEBPEPERKRSFVEMVNLNRKSGQGYVEMTWG 61
DB 34 ENGIRKAPL-----VDPATKYNQVATAVEPLSNYMDMS---YYGSIISIG 74
QY 62 SPPTQNLIVDTGSSNFAVGA-----APHPFLHRYRQQLSTYDIAKGVV 113
DB 75 TPQNPLVLPDTSSNLMWASTYCQSOACTNHPL---FNPSSQSTYSSNQQPSLQYGT 130
QY 114 GKKEGELGTDVSIHGPNTVFRANIAITAESDKFPIGNSN-----WEGILGLAYAEIAR 168
DB 133 GSITGLIGLYTVI---QNVAIQOBERGLSETP---GTNPFYVAGPFDGILGLAYPSIA- 182
QY 169 PDDSLPEPFDLSVKQTHVPNLPSLQLCAGAPLQSEVLASVGSMTIIGIDHSLYTGSL 228

DB 183 -VGATTVMGQMGO-----NLNQPI--FGFVLSGQS--SQNGGEVAFGVQDVQVYTSQI 233
QY 229 WYTPPIRREMYEVIIVVEINGD--LKWDCKRYNDKSIYDSGTTNLRPKVFEAAV 285
DB 224 YMTPTSETVYQIGIOGFSINGQATGWCSGOC-----QALVDGTSLTLPAQVFSLSI 287
QY 286 KSIAKASSTKPPDGMGLGEOLVCMQAGTTPMNI--FPVISLYLMG-----EVTNQ 334
DB 288 QSIGAQDQD-----GQYVSCS-----NIQNLPTISFTISGVSFPLPSPAYVLCQ 333
QY 335 S-----FRITILPOQYLAREPVEDVATSDCCYKPAISQSGSTGVMGAVIMEGYVVFDR 387
DB 334 SSGYTTGIMPTVLPQSGQGL-----WILGDVFLREYVSVDL 372
QY 388 ARKIRGFAVSA 398
DB 373 GNNQVGFATAA 383

RESULT 6

S19682
pepsin A (EC 3.4.23.1) 4 precursor - Japanese macaque
N.Alternate names: pepsinogen A isozyme 4
C.Species: Macaca fuscata (Japanese macaque)
C.Date: 22-Nov-1993 #sequence_revision 19-Oct-1995 #text_change 16-Aug-2004
C.Accession: S19682; S16065
R.Kageyama, T.; Tanabe, K.; Koizumi, O.
Eur. J. Biochem. 202, 205-215, 1991
A.Title: Development-dependent expression of isozymogens of monkey pepsinogens and struc
A.Reference number: S19681; MUID:92037645; PMID:1935977
A:Accession: S19682
A:Molecule type: mRNA
A:Residues: 1-388 <KAG>
A:Cross-references: UNIPROT:P27678; EMBL:X59753; NID:G38070; PID:CAA42425.1; PID:G38071
A:Note: parts of sequence, including amino ends of pepsinogen and activation intermediat
C.Comment: This is a minor component of pepsin at all post-partum stages.
C:Comment: Although two-step activation is observed, activation is predominantly a one-
C:Superfamily: Pepsin
C:Keywords: aspartic proteinase; gastric juice; hydrolyase; phosphoprotein; protein diges

F.1-15/Domain: signal sequence #status predicted <SIG>
F.15-388/Product: pepsinogen A 4 #status experimental <APT>
F.16-62/Domain: activation peptide #status experimental <APR>
F.63-388/Product: pepsin A 4 #status experimental <ENZ>
F.38-39/Cleavage site: Leu-Lys (pepsin) #status experimental
F.62-63/Cleavage site: Leu-Ile (pepsin) #status experimental
F.94/277/Active site: Asp #status predicted
F.107-112,268-272,311-344/Diulfide bonds: #status predicted
F.130/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 13.2%; Score 302.5; DB 1; Length 388;
Best Local Similarity 27.6%; Pred. No. 1e-16;
Matches 107; Conservative 64; Mismatches 133; Indels 83; Gaps 17;

QY 27 DEBPEPERKRSFVEMVNLNRKSGQGYVEMTWGSPPTLNIIVDTGSSNFAVGAAPRP 86
DB 64 DQOPLR-----NYLVV-----EYFGTIGIGIPRONFTVVDTGSSNLMV---PQV 105
QY 87 PL-----HRYRQQLSTYDIAKGVVPTQKMEGELGTDVSIHGPNTVFRANI 139
DB 106 YCYSLACMDHNLFPNDDSTYRATKTVSITGTGSMGILGIDYTVKV---GGISDTNQI 162
QY 140 AAITESDK-FPINGSNMEGILGLAYAEIARPPDLSLPPFDLSVKQTHV-PNLPSLQLCGA 197
DB 163 FGLSETPGFPLFYAPFDGILGLAYPSIS--SSGATPVEDNTMNQRLVSQDLFSVYLSAD 220
QY 198 GFLNQSVELASVGSMTIIGIDHSLYTGSLTYTPIRREMYEVIIVVEINGDGL--KM 255
DB 221 ---DQS-----GSVVYFGIDSSYTGSLMWVPSVSGVQISVDSITMGKTYACK 270
QY 256 DCKENYDKSIYDSGTTNLRPKVFEAAVKSIAKASSTKPPDGMGLGEOLV-CWQAGT 314
DB 271 GC-----QALVDGTSLTLGPTSPANIQSDIGASNSND-----GEMVVSQSAIS 316

QY 315 TPWNIFFVYSLXMGELTNGSGFRITLLEPOY-LRPVEDVATSGDDCYK-----FAISQSS 368
Db 317 LPDVF-----TINGVQYPLPPSAVYLIQSQSCSTSGFGMDVPTESG 368
QY 369 TGTWGAIVMEGFYVFPDRARKIGFA 395
Db 359 ELWILGDVFIRQYFTVFDNRANQVGLA 385

RESULT 7

A39314
gastriecin (EC 3.4.23.3) precursor - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 16-Aug-2004
C/Accession: A39314
R/akade, E.; Tanji, M.; Ichinose, M.; Goto, S.; Miki, K.; Kurokawa, K.; Ito, H.; Kageya
J. Biol. Chem. 266, 22436-22443, 1991
A/Title: Purification, characterization, and amino acid sequences of pepsinogens and pep
A/Reference number: A39314; MUID:92042186; PMID:1939266
A/Accession: A39314
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-384 <YAK>
A/Cross-references: UNIPROT:Q91322; GB:M73750; NID:g213687; PIDN:AAA49530.1; PID:g213688
C/Superfamily: Pepsin
C/Keywords: aspartic proteinase; hydrolase; protein digestion

Query Match 13.2%; Score 302; DB 2; Length 384;
Best Local Similarity 24.5%; Pred. No. 1.1e-16;
Matches 105; Conservative 65; Mismatches 147; Indels 112; Gaps 17;
QY 3 HGIRLPRLSGAGAPLGLINLETDEPERGR--GSFEMVDNRKSGCGCYVEMTV 60
Db 35 HGIRKAV-----VDATKYNNRATRAEPLANYMDMSYGEISL 73
QY 61 GSPPTQNTLIVDTGSSNFAVGAAPHPL-----HRYVQRQLSSTRDLRKGVVPTQY 113
Db 74 GTPQNFVLVFDTGSSNLWV---PSTYCQSQACTNHPQNPSSSSYSNQQQFSLQYCT 130
QY 114 GKMEGLGTDVLSIPHGPNTVRAPIA-----AITSDEXFINGSNWEGILGLAYAE 165
Db 131 GSITGLIGDYVQI-----QNTAISQGEFGLSVTEPGNFVY-AQFDGILGLAAPS 180
QY 166 IARPDLSPEFPDLSVQKQTHVN-LFSLQLCGAGFPLNQEVLASVGSMTIIGIDHSLY 224
Db 181 IAA-EGGATVWQGMQQLINQPLFAFYLSSQOQNSQ-----GSEVAFGVDQNY 230
QY 225 TGSMTPTPIRREMYEVIIIVVEINGQD--LMDCKEYNDKSIYDSGTTNLRLLPKVFE 281
Db 231 SQGIWVTPVTSBTYQIGIQGSPVNGQATGWCSCG-----QGIYDGTSLTAPQSVF 284
QY 282 EAAVKSIRKAASTEKFPDGFMLGEOLY-CWQAGTTPWNIFFVY-----SLYMGSEVT 332
Db 285 SLMQSIGAQDON-----QYAVSCSNITQSPITTSFTISGVSPPLPSAAYVLQNS 336
QY 333 NO--SFRTIILPQYLRPEVDVATSGDDCYKFAISQSGSTGTWGAIVMEGFYVFPDRAR 389
Db 337 GYCTIGIMFTYLPSONGQPL-----WILGDVLRQYISVYDIGN 375
QY 390 KRIGFAVA 398
Db 376 NOVGFRAAA 384

RESULT 8

pepsin A (EC 3.4.23.1) precursor - chicken
N/Alternate names: pepsinogen A
C/Species: Gallus gallus (chicken)
C/Date: 18-Apr-1984 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
C/Accession: J06370; A00984
R/Sakamoto, N.; Saita, H.; Yasugi, S.

Biochem. Biophys. Res. Commun. 250, 420-424, 1998
A/Title: Analysis of temporal expression pattern and cis-regulatory sequences of chicken
A/Reference number: J06370; MUID:98440813; PMID:9753645
A/Accession: J06370

A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-382 <SAK>
A/Cross-references: UNIPROT:Q9PRG9; GB:AB025281; NID:g4589837; PIDN:BA476891.1; PID:g4589837
R/Baudys, M.; Kostka, V.
Eur. J. Biochem. 136, 89-99, 1983
A/Title: Covalent structure of chicken pepsinogen.
A/Reference number: A00984; MUID:84004412; PMID:6617663
A/Accession: A00984
A/Molecule type: protein
A/Residues: 16-87, 'S', 89-382 <BAU>
C/Superfamily: Pepsin
C/Keywords: aspartic proteinase; gastric juice; glycoprotein; hydrolase; protein digestion
F/16-57/Domain: activation peptide #status experimental <APT>
F/58-382/Product: pepsin A #status predicted <MAT>
F/92,275/Active site: Asp #status predicted
F/105-110,266-270,305-338/Disulfide bonds: #status experimental
F/128/Binding site: carbonylate (Asn) (covalent) #status experimental

Query Match 13.2%; Score 301; DB 1; Length 382;
Best Local Similarity 24.0%; Pred. No. 1.3e-16;
Matches 88; Conservative 68; Mismatches 126; Indels 84; Gaps 13;
QY 54 YVEMTVGSPPTQNTLIVDTGSSNFAVGAAPHPL-----HRYVQRQLSSTRDLRK 106
Db 74 YGIGTISGTPODPTVIFDTGSSNLWV---PSTYCQSSACSNKRDPKSSITVSTNET 130
QY 107 YVVPYITQKMEGLGTDVLSIPHGPNTVRAPIAITSQD-K-FPINGSNWEGILGLAYAE 165
Db 131 VYIAYGTGSMGSLIGYPTVAV---SSIDVQNOIFGSETEPGSFYVCNFDGILGLAFPS 187
QY 166 IARPDLSPEFPDLSVQKQTHVN-PNLSLQLCGAGFPLNQEVLASVGSMTIIGIDHSLY 224
Db 188 IS--SSATVTFVDMQMSQHLVAQDLFSVYLSKQ-----ETGSEVFLFGGIDPNYT 235
QY 225 TGSMTPTPIRREMYEVIIIVVEINGQD-L-MDCKEYNDKSIYDSGTTNLRLLPKVFE 282
Db 236 TKGIYVWPLSAETVWQITMDRVTVGKRYVACFPCT-----QAIYDGTSLVMPGAGAN 289
QY 283 AAVKSIKAASTP-----KFPDGFMLGEOLYCWQAGTTPWNIFFVYSLXMGELTNGS 335
Db 290 RIIRKDLGVSSDGIISCDISKLDP-----VTFPHNGHA----- 322
QY 336 FRITILPQYLRPEVDVATSGDDCYKFAISQSGT-----VWGAIVMEGFYVFPDRAR 389
Db 323 -----FTLPASAVYLVNEDSCMLGFENMGTPIELGEQWILGDVFIRYVYVFDNRAN 373
QY 390 KRIGFA 395
Db 374 NKVGLS 379

RESULT 9

A34401
cathepsin E (EC 3.4.23.34) precursor - human
C/Species: Homo sapiens (man)
C/Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 16-Aug-2004
C/Accession: A42038; A34401; S35663; S34467; A34643; B31643
R/Azuma, T.; Liu, W.; Vander laan, D.J.; Bowcock, A.M.; Taggart, R.T.
J. Biol. Chem. 267, 1609-1614, 1992
A/Title: Human gastric cathepsin E gene. Multiple transcripts result from alternative po
A/Reference number: A42038; MUID:92112877; PMID:1370478
A/Accession: A42038
A/Molecule type: DNA
A/Residues: 1-396 <AZU>
A/Cross-references: UNIPROT:P14091; GB:M84424; GB:M82847; NID:g181203; PIDN:AAA52300.1; I
R/Azuma, T.; Fals, G.; Mohandas, T.K.; Couvreur, J.M.; Taggart, R.T.
J. Biol. Chem. 264, 16748-16753, 1989


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Matches 97; Conservative 63; Mismatches 135; Indels 66; Gaps 13;
QY 54 YVETKVGSPQTLNLTVDGSSNFAVGAAPHF-----LHRYRQRLSSTYRDLKRG 106
DB 75 YFGTISIGPPQDFVITFDTGSSNLMV---PSTYCSLALCKHRFNEDSSTYQGSRT 131
QY 107 VVVPYTGKMEGELGTDLVSI-PHGPNVTVRANIAAITESDKFFINGSMWEGILGLAVAEI 166
DB 132 LSTYTGSTMTGILGIDYTVKVGSLBDTQIFGLSTEPSLTFP--APFDIITGLAAPSII 189
QY 167 ARPDLSLEPFDLSLVKQTHV--PNLFSLQLCGAGFPLNOSSEVLASVGSMITIGIDHSLYT 225
DB 190 SSSDAT--PVFDNMNNEGVLVSQDLFSVYLLSSD-----EKSGLVWFSGGIDSSYIT 237
QY 226 GSLWTPFIRREMYEVIIIVREINGDLK--DKEYNYDKSYDSTGTLRLPKVFEA 283
DB 238 GSLMWPVSYEGVQIOTWDSVINGETIACADSC-----QATVDTSSTLTGP---TS 287
QY 284 AVKSIKAASSTKEPFDGFWLGEOLV-CWQAGTTPMNIIPVYISLVLMGEVTVNSFRITILP 342
DB 288 AISNIQSYIGASK-----NLGSENVISCSAIDSLPDIYF-----TING 325
QY 343 QQYLRPEVDVATSDDDCYKRAISQSSGT-----VNGAVIMEGFYVFPDRARRIGFAV 396
DB 326 IQYPLPASAVYLKEDDDCTSGLEGANVDYTGELMILGIDVFIRQYFTVPDRANNQGLAA 385
QY 397 S 397
DB 386 A 386

RESULT 12
A43356
cathepsin B (EC 3.4.23.34) precursor - guinea pig
N:Alternate names: eythrocyte membrane aspartic proteinase; slow-moving proteinase
C:Species: Cavia porcellus (guinea pig)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Aug-2004
C:Accession: A43356
R:Kageyama, T.; Ichinose, M.; Tsukada, S.; Miki, K.; Kurokawa, K.; Koiwai, O.; Tanji, M.
J. Biol. Chem. 267, 16450-16459, 1992
A:Title: Gastric procathepsin B and progastricrin from guinea pig. Purification, molecu
A:Reference number: A43356, MUID:92355614; PMID:1644629
A:Accession: A43356
A:Molecule type: mRNA
A:Residues: 1-391 <RAG>
A:Cross-references: UNIPROT:P25796; GB:W88653; NID:9191294; PIDN:AAA7052.1; PTD:9191295
A>Note: sequence extracted from NCBI backbone (NCBIN:110763, NCBI:P110769)
C:Superfamily: Pepsin
C:Keywords: aspartic proteinase; hydrolase; membrane protein

Query Match 12.9%; Score 296; DB 2; Length 391;
Best Local Similarity 26.9%; Pred. No. 3.4e-16;
Matches 98; Conservative 64; Mismatches 130; Indels 72; Gaps 16;
QY 54 YVETKVGSPQTLNLTVDGSSNFAVGA---AHPFLHRYRQRLSSTYRDLKRGYV 109
DB 75 YFGTISIGPPQDFVITFDTGSSNLMVSVCTSPACQTHVFRHSLSSTYREVNSFSRI 133
QY 110 PYTGKMEGELGTDLVSI-PHGPNVTVRANIAAITESDKFFINGSMWEGILGLAVAEIAR 169
DB 134 QYGTSLTIGIIGADQVSV--EGLTVVGQGFGEVDEPGKTFPH--AFPDIIITGLSPSLAA-- 190
QY 170 DDSLPEPFDLSLVKQTHVRLPSQLCGAGFPLNOSSEVLASVGSMITIGIDHSLYTSLW 229
DB 191 -GGVTPVFDNMNAQ---NLVALPM---FSVYMSNPGSGSELTFEGYDP SHFSGSLN 241
QY 230 YTPIRREMYEVIIIVREINGDLKMDKEYNYDKSYDSTGTLRLPKVFEAAYVSIK 289
DB 242 WVPVTKAVYQWQALDGIQV--DSVMFSE---GCQALVDGTSLTGP---PEKIKIQ 293
QY 290 AASSTKEPFDGFWLGEOLV-CWQAGTTPMNIIPVYISLVLMGEVTVNSFRITILPQ 344
DB 294 BALGATVYDEGV---SVQC-----ANLNMMLDVT---FLINGVPTILNPTA 333
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QY 345 YLRPEVDVATSDDDCYKRAISQSSGT-----TWGAVIMEGFYVFPDRARR 391
DB 334 Y--TLIDFPDQMCV-----STFEGLEIQPPAGFWLIGDVFTRQFAVADRGNNR 383
QY 392 IGFA 395
DB 384 VGLA 387

RESULT 13
KRTD
cathepsin D (EC 3.4.23.5) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-2004
C:Accession: S13111; C1918; Q01177; P00222
R:Birch, N.P.; Loh, Y.P.
Nucleic Acids Res. 18, 6445-6446, 1990
A:Title: Cloning, sequence and expression of rat cathepsin D.
A:Reference number: S13111; MUID:91057150; PMID:2243802
A:Accession: S13111
A:Molecule type: mRNA
A:Residues: 1-407 <BIR>
A:Cross-references: UNIPROT:P24268; EMBL:X54467; NID:955881; PIDN:CAA8349.1; PTD:955882
R:Yonezawa, S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartenack, J.A.; Tang, J.
J. Biol. Chem. 263, 16504-16511, 1988
A:Title: Structures at the proteolytic processing region of cathepsin D.
A:Reference number: A92681, MUID:89034127, PMID:3182800
A:Accession: C31918
A:Molecule type: protein
A:Residues: 134-152, 'T', 164-170 <YON>
R:Fujita, H.; Tanaka, Y.; Noguchi, Y.; Kono, A.; Himeno, M.; Kato, K.
Biochem. Biophys. Res. Commun. 179, 190-196, 1991
A:Title: Isolation and sequencing of a cDNA clone encoding rat liver lysosomal cathepsin
A:Reference number: Q01177; MUID:91354249; PMID:1883350
A:Accession: Q01177
A:Molecule type: mRNA
A:Residues: 1-14, 'A', 16-204, 'N', 206-261, 'N', 263-407 <FUJ>
A:Accession: P00222
A:Molecule type: protein
A:Residues: 65-74, 118-127, 165-174 <FUJ>
A:Experimental source: liver
C:Function: Cathepsin D in rat liver lysosome occurs as a mixture of both a single chain f
A:Description: limited specificity endopeptidase
A:Pathway: intracellular protein degradation
C:Superfamily: Pepsin
C:Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-64/Domain: propeptide #status predicted <PRO>
F:65-407/Product: cathepsin D, 43K single-chain form #status predicted <MA7>
F:65-144/Product: (or 65-165) cathepsin D 12K light chain #status predicted <MA2>
F:65-147/Product: cathepsin D 9K light chain #status predicted <MA4>
F:118-407/Product: cathepsin D 34K heavy chain #status predicted <MA5>
F:165-407/Product: (or 166-407) cathepsin D 30K heavy chain #status predicted <MA3>
F:91-160, 110-117, 281-285, 324-361/disulfide bonds: #status predicted
F:97, 290/active site: Asp #status predicted
F:134, 258/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.9%; Score 296; DB 1; Length 407;
Best Local Similarity 25.6%; Pred. No. 3.6e-16;
Matches 112; Conservative 77; Mismatches 152; Indels 96; Gaps 19;
QY 5 IRLPLR-----SGCGAPLGL-----EINLREDEPPEPGRGSEVENVNLRG 48
DB 22 IRLPLRKTTSIRRTWTEVGSVEDILKGPITKXSMOSSPRTKEP-----VSEILKN 73
QY 49 KSGGQYVETKVGSPQTLNLTVDGSSNFAVGAAPHF-----HRYRQRLSSTYRD 102
DB 74 YLDAQYVEIGITPPQDFVITFDTGSSNLMVPSIHKCLDIDACWYHKKNSDKSSTYV 133
QY 103 LKRGVYVYTGKMEGELGTDLVSI-PHGPNVTVRANIAAITESDKF-----ING 152
```


J. Biol. Chem. 265, 17031-17038, 1990
 A;Title: Structure and development of rabbit pepsinogens. Stage-specific zymogens, nucle
 A;Reference number: A38302; MUID:91009127; PMID:2129536
 A;Accession: D38302
 A;Status: Preliminary
 A;Molecule type: mRNA
 A;Residues: 1-387 <XAG>
 A;Cross-references: UNIPROT:P28713; GB:M59235; GB:J05638
 C;Superfamily: Pepsin
 C;Keywords: aspartic proteinase; hydrolase; phosphoprotein; protein digestion

Query Match 12.9%; Score 295; DB 2; Length 387;
 Best Local Similarity 26.1%; Pred. No. 4.1e-16;

Matches 97; Conservative 65; Mismatches 123; Indels 86; Gaps 14;

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QY 54 YVEMTVGSPPTLNLIVDTGSSNFVGAAPHP-----LHRYQRLSTYRDLKRG 106
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 75 YFETISIGTPPODFTYIFDTGSSNLWV---PSTYCSSLACALHKRFNPEDSSTYQCTSET 131
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 107 VVVPYTOGKKEBELGTDLVSIPIGPNVTYRANIAITESDKPF-----INGSNWE 156
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 132 LSTITGTGSMGTGLGIDTV-----KVGSIEDTNQIFGLSKTEPGLTFLFAPPD 179
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 157 GILGLAYABIAIPDDSLBPFDLSLVKQTHV-PNLFSLQLCGAGFPLNOSVLAAYGSGMI 215
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 180 GILGLAYPSISSDAT--PVFDNMNNEGVSQDLFSVYLSDD-----EKGSLYM 227
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 216 IGGIDHSLYTGSLMYPIREMYEVIYRVEINGODLKM--DCKEYNDKSIYDSGTTN 273
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 228 FGGIDSSYYTGLNWPVSVYEGWQITMDSVISINGETIACADSC-----QAIIVDTGTSL 281
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 274 LRLPKVFEAAVYSIKAASTEKFPDGFMLGEOLV-CWQAGTTPMNIIPVVISLYLMGEVT 332
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 282 LIGP-----TSAINISQSYIGASK---NLGENVISCASIDSLPDIYF----- 321
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 333 NOSFRITLIPQOYLRFVEDVATSQDDCYKFAISQSSTGT-----VMGAVIMEGFYVVD 386
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 322 -----TINGIQYPLPASAYILKEDDDCTSGLEGMNVDTYTGELMTLIGDVFIRQYFTVVD 375
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 387 RARKRIGFAVS 397
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 376 RANNQGLAA 386
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Search completed: August 22, 2005, 00:25:10
 Job time : 61 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2005, 00:54:10 ; Search time 1103 Seconds

(without alignments)
2550,468 Million cell updates/sec

Title: US-10-726-967a-84

Perfect score: 2288

Sequence: 1 TQHGIRLPRLSGLGAPLGL.....FTYLMEDCGINIPQTDST 433

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DBV=xlp
-O=/cg2n_1/USPRO.spool.p/US10726967/runat.19082005.201241.29685/app.query.fasta_1.583
-DB=Published Applications NA -QWMT=faaetap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=ptc -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10726967 @CGN 1.1 723 @runat.19082005.201241.29685
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -NAIT -DSPBLOCK=100
-LONGLOG -DEVI TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:*

- 1: /cg2n_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cg2n_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cg2n_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cg2n_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 5: /cg2n_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 6: /cg2n_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 7: /cg2n_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 8: /cg2n_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 9: /cg2n_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 10: /cg2n_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 11: /cg2n_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 12: /cg2n_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 14: /cg2n_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 15: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 17: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 18: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 19: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 20: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 21: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 22: /cg2n_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 23: /cg2n_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 24: /cg2n_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*
- 25: /cg2n_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 26: /cg2n_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2267	99.1	1371	19	US-10-281-092-7
2	2267	99.1	1503	24	US-11-089-918-1
3	2267	99.1	1503	24	US-11-090-866-1
4	2267	99.1	1503	24	US-11-069-377-1
5	2267	99.1	1503	24	US-11-090-872-1
6	2267	99.1	1506	15	US-10-214-932-5
7	2267	99.1	1506	15	US-10-281-092-5
8	2267	99.1	1527	19	US-10-275-339A-6
9	2267	99.1	1542	15	US-10-322-684-1
10	2267	99.1	2070	18	US-10-652-927-3
11	2267	99.1	2070	18	US-10-652-830-3
12	2267	99.1	2070	19	US-10-652-045-3
13	2267	99.1	2070	21	US-10-940-867-3
14	2267	99.1	2348	24	US-11-089-918-4
15	2267	99.1	2348	24	US-11-090-866-4
16	2267	99.1	2348	24	US-11-069-377-4
17	2267	99.1	2348	24	US-11-090-872-4
18	2267	99.1	2526	22	US-10-466-358-1
19	2267	99.1	2526	22	US-10-466-391A-1
20	2267	99.1	3252	9	US-09-796-264-1
21	2267	99.1	3252	9	US-09-845-226-1
22	2267	99.1	3252	9	US-09-795-903A-1
23	2267	99.1	3252	14	US-10-032-818-1
24	2267	99.1	3252	19	US-10-820-953-1
25	2267	99.1	3252	20	US-10-773-754-1
26	2267	99.1	5832	19	US-10-721-693-18
27	2267	99.1	5832	20	US-10-852-957-18
28	2267	99.1	5876	20	US-10-723-860-5006
29	2267	99.1	5876	17	US-10-159-942-4
30	2267	99.1	5878	20	US-10-723-860-284
31	2267	99.1	5878	21	US-10-956-157-1778
32	2267	99.1	16080	24	US-11-089-918-48
33	2267	99.1	16080	24	US-11-090-866-48
34	2267	99.1	16080	24	US-11-069-377-48
35	2267	99.1	16080	24	US-11-090-872-48
36	2262	98.9	1368	18	US-10-627-473-1
37	2262	98.9	2070	9	US-09-794-927-3
38	2262	98.9	2070	9	US-09-795-847-3
39	2262	98.9	2070	9	US-09-794-748-3
40	2262	98.9	2070	9	US-09-794-748-3
41	2262	98.9	2070	9	US-09-794-925-3
42	2262	98.9	2070	9	US-09-681-443-3
43	2262	98.9	2070	10	US-09-908-943A-1
44	2262	98.9	2070	10	US-09-869-414-3
45	2262	98.9	2070	10	US-09-548-366-3

ALIGNMENTS

RESULT 1
US-10-281-092-7
; Sequence 7, Application US/10281092
; Publication No. US20040121947A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Arun K.
; APPLICANT: Tang, Jordan J.N.
; APPLICANT: Bilcer, Geoffrey
; APPLICANT: Chang, Manpin
; APPLICANT: Hong, Lin
; APPLICANT: Koelsch, Gerald E.
; APPLICANT: Loy, Jeffrey A.
; APPLICANT: Turner, Robert T., III
; APPLICANT: Devaunadrum, Thippeswamy
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
; ACTIVITY AND METHODS OF USE THEREOF

```

/ FILE REFERENCE: 2932.1001-004
/ CURRENT APPLICATION NUMBER: US/10/281.092
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: US 10/032, 818
/ PRIOR FILING DATE: 2001-12-28
/ PRIOR APPLICATION NUMBER: PCT US01/50826
/ PRIOR FILING DATE: 2001-12-28
/ PRIOR APPLICATION NUMBER: US 60/258, 705
/ PRIOR FILING DATE: 2000-12-28
/ PRIOR APPLICATION NUMBER: US 60/275, 756
/ PRIOR FILING DATE: 2001-03-14
/ PRIOR APPLICATION NUMBER: US 60/335, 952
/ PRIOR FILING DATE: 2001-10-23
/ PRIOR APPLICATION NUMBER: US 60/333, 545
/ PRIOR FILING DATE: 2001-11-27
/ PRIOR APPLICATION NUMBER: US 60/348, 464
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/348, 615
/ PRIOR FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/390, 804
/ PRIOR FILING DATE: 2002-06-20
/ PRIOR APPLICATION NUMBER: US 60/397, 557
/ PRIOR FILING DATE: 2002-07-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 1371
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: promemapsin 2-T1
/ US-10-281-092-7

Alignment Scores:
Pred. No.: 7 42e-269 Length: 1371
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 19 Gaps: 0

US-10-726-967a-84 (1-433) x US-10-281-092-7 (1-1371)
QY 1 ThrGlnHiGlyTLeaArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
DB 70 ACCCAAGCAAGGATCCGGCTGCCCTCGCCAGCGGCTGGGGGCCCCCTGGGCTG 129
QY 21 GluIleAsnLeuGluThraSpGluGluProGluGluProGlyArgArgGlySerPheVal 40
DB 130 CGGCTGCCCGGGAAGACCGACGAGAGCCCGGAGAGCCCGGCGGAGGGGCGAGCTTTGTG 189
QY 41 GluMetValAspAsnLeuArgGlyLySerSerGlyGlnGlyTyrTyrValGluMetThrVal 60
DB 190 GAGATGGTGGACAACCTGAGGGGCAAGTGGGGCAGGGCTACTAGTGAAGTGAACCTG 249
QY 61 GlySerProGlnThraLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
DB 250 GGCACCCCCCGACACGCTCAACATCTGGTGTATACAGACGACGATTAACCTTGCACTG 309
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
DB 310 GGTGTGCCCCCCCCCTTCTCTGATGCTACTACAGAGCGAGTGTCCAGACATAC 369
QY 101 ArgAspLeuArgGlyValTyrValProTyrThrGlnGlyLysTrpGluGlyGlyLeu 120
DB 370 CGGGACCTCCGGAGAGGTGTGTATGTGCTTACACCCAGGGCAAGTGGAGAGGGAGCTG 429
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValAlaAsnIleAla 140
DB 430 GGCACCGACCTGTGATGATCCCCCATGCGCCCAACGTCATGTGCGTGCACCATTTGCT 489
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160

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DB 490 GCCATCAGTGAATGACAAAGTTCTTCAACAGGCTCCACCTGGAAAGCATCTGGCG 549
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180
DB 550 CTGGCTTATGCTGAATGGCAAGGCTGACGATCCCTGGAGCCCTTTCTTGTGACTCTCG 609
QY 181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro 200
DB 610 GTAAGCAGACCCAGGTTCCCAACCTCTTCCCTGAGCGTTTGTGCTGCTTCC 669
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyTyrIleAsp 220
DB 670 CTCAACCGATGTGAAGTCTGCTGCTGTGCGAGGAGCATGATCATTTGAGATGAC 729
QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrProIleArgArgGluTyrTyrGlu 240
DB 730 CACTGCTGTACAGAGGAGCTCTGATATACCCATCCGAGGAGGTGTATATGAG 789
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLysGluTyr 260
DB 790 GTCATCATTTGCGGGTGGAGATCAATGACAGGATCTGAATAATGACTGCACAGAGTAC 849
QY 261 AsnTyrAspLysSerIleValAspSerGlyTyrThrAsnLeuArgLeuProLysVal 280
DB 850 AACTATGACAAAGACATTTGGACAGTGGACCAACCACTTGTGTTGCCCAAGAAAGTG 909
QY 281 PheGluAlaAlaValLysSerIleLysAlaAlaSerSerThrGluLysPheProAspGly 300
DB 910 TTGTAACTGCAAGTCAATCCATCAACAGGAGCTCTCCCAAGAAAGTTCCCTGATGT 969
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyTyrThrProTrpAsnIlePhe 320
DB 970 TTCTGGCTAGAGAGCAGCTGTGTCTGGCAAGCAGCAACCCCTTGGAAACATTTTC 1029
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB 1030 CAGTATCTCACTCACTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 1089
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
DB 1090 CTTCGCGAGCAATATCTGCGGCGGAGTGGAAAGTGTGGCAACGTCCTTGTAC 1149
QY 361 LysPheAlaIleSerGlnSerSerThrGlyTyrValMetGlyAlaValIleMetGlyGly 380
DB 1150 AAGTTGCCATCTCAAGTATATCACGGGCACTGTATGGAGCTGTATCATGAGAGGC 1209
QY 381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
DB 1210 TTCTACGTTGTCTTTGATCGGGCCGAAACGAATTGGCTTGTCTGTACGCCCTTGCCAT 1269
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1270 GTGCACAGTAAAGTTCAGAGCGGACGGGTGGAAGGCCCTTTTGTGACCTTGGACATGGA 1329
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGlnSerThr 433
DB 1330 GACTGTGGCTACACATTCACAGACAGATGAGTCAACC 1368

RESULT 2
US-11-089-918-1
/ Sequence 1, Application US/11089918
/ Publication No. US20050164327A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, John P.
/ APPLICANT: Baal, Gurigal
/ APPLICANT: Doane, Minh Tam
/ APPLICANT: Frigon, Normand
/ APPLICANT: John, Varghese
/ APPLICANT: Power, Michael
/ APPLICANT: Sinha, Sukanto
/ APPLICANT: Tatauro, Gwen
/ APPLICANT: Tung, Jay

```

```
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEW2C9
CURRENT FILING DATE: 2005-03-25
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 1999-12-24
PRIOR FILING DATE: 1999-02-10
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1503
TYPE: DNA
ORGANISM: Homo sapiens
US-11-089-918-1

Alignment Scores:
Pred. No.: 8,54e-269 Length: 1503
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0
DB: 24

US-10-726-967a-84 (1-433) x US-11-089-918-1 (1-1503)

QY 1 ThrglnHlglyYlIeargLeupProleuAgsSerGlyLeuGlyValaProluenglyLeu 20
DB 64 ACCCGACAGCGGCAATCCGGCTGCGCCCGACGCGCTGCGGCGGCGCGCGCGCGCGCGCGCG 123
QY 21 GluIleAsnLeuGluThraPglugluProlGluGluProlGlyValaProlGlySerPheVal 40
DB 124 CGGCTCCCCGGAGACCGACAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 183
QY 41 GluMetValaAspAsnLeuArglyLySerGlyValGlyValGlyValGlyValGlyValGlyVal 60
DB 184 GAGATGCTGACCACTGAGCGGCGCAAGTCCGGGCAAGGCGCTACTACGAGATGACCGCTG 243
QY 61 GlySerProProlGlnThraLeuAnlleuValaAspThrGlySerSerAsnPheAlaVal 80
DB 244 GGCAGCGCGCGCGCGCGCGCTCAACATCTGCTGATACAGGCGAGCTTGTGACGCTG 303
QY 81 GluAlaAlaProlAspPheLeuHlsArgTyThrGlnaArgGlnLeuSerSerThrTy 100
DB 304 GGTGCTGCGCGCGCGCGCGCTTCTGCTGCTACTACAGAGCGAGCTGTCCACAGACTAC 363
QY 101 ArgAspLeuArglySerGlyValTyValProTyThrGlnGlyLySerTrpGluGlyLeu 120
DB 364 CGGAGCTCCGGAAGGCTGTATGCTCCTACACCGAGGCAAGTGGAGAGGCGAGCTG 423
QY 121 GlyThraPleuValSerlleProlHlsGlyProAsnValThraValaAlaValaAla 140
DB 424 GGCACCGACCTGGTAAAGCATCCCCCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 483
QY 141 AlaIleThrgIuSerAspLyPhePheIleAsnGlySerAsnTrpGluGlyIleuGly 160
DB 484 GCCATCACTAATCAACAGAGTTCTTCAACAGGCTCCCACTCGGAGAGGCACTCTGGG 543
QY 161 LeuAlaTyraIagluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB 544 CTGGCCATGCTGAGATGCGCAAGCGCTGACGACCTCCCTGAGCCTTCTTGACTCTCTG 603
QY 181 ValIyGlnThraHlsValaProlAsnLeuPheSerLeuGlnLeuGlySerGlyValaGlyPhePro 200
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DB 604 GTAAAGCAGACCCAGTTCACCACTTCTCCCTGACAGCTTGTGTGCTGCTTCC 663
QY 201 LeuAsnGlnSerGluValaLeuAlaSerValGlyGlySerMetIleIleGlyIleAsp 220
DB 664 CTCAACAGCTGAGAGTCTGCTGCTGCTGAGAGAGCAATGATCATTTGAGAGTTCAC 723
QY 221 HisSerLeuTyThrGlySerLeuTrpTyThrProIleArgArgGluTrpTyTrGlu 240
DB 724 CACTGCTGTACAGAGAGCTCTCTGTATACCCACCGCGGAGAGTGTATATAG 783
QY 241 ValIleIleValaArgValaGluIleAsnGlyGlnAspLeuValMetAspCysIleGlyTr 260
DB 784 GTGATCATTTGGCGGGTGGATCATAGACAGGATCTGAAATGAGACTGCAAGAGATAC 843
QY 261 AsnTyraAspLySerIleValaAspSerGlyThrThraAsnLeuArgLeuProIleVal 280
DB 844 AACTATGACAGAGCATTTGTGACAGTGGCACACCAACCTTCTTCCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValaIleSerIleValaAlaSerSerThrGluLyPheProAspGly 300
DB 904 TTGAAAGCTGACGTAAATTCATCAAGGCAAGCTCTCTCAAGAGAAATTCCTGATG 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
DB 964 TTCTGGCTAGAGAGACAGCTGGTGTGTGCGAAGCAGACCACTTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTyThrLeuMetGlyGlyValaThraAsnGlnSerPheArgIleThrIle 340
DB 1024 CCAGTCATCTCACTCTACTATATGGGTAGGTATACCAACAGTCTTCCGATCACCATC 1083
QY 341 LeuProGlnGlnTyThrLeuArgProValaGluAspValaIleThrSerGlnAspAspCysTy 360
DB 1084 CTTCGCGAGCAATACCTGGCGGCAAGTGTGCGCAAGTGTGCGCAAGTGTGCGCAAGTGTG 1143
QY 361 IysPheAlaIleSerGlnSerSerThrGlyThrValaMetGlyAlaValaIleMetGlyGly 380
DB 1144 AAGTTGGCATCTCAAGATCATCCAGCGGCACTGTTATGGAGCTGTATATCAAGAGGCG 1203
QY 381 PheTyraValaPheAspArgAlaArglyAsaGlyIleGlyPheAlaValaSerIleCysHls 400
DB 1204 TTCTACGTTGCTTGTGATCGGCGCGCAAAACAAATGGCTTTGCTGCTGCGCTTGCCT 1263
QY 401 ValHlsAspGluPheAspThrAlaAlaValaGluGlyProPheValaThraLeuAspMetGlu 420
DB 1264 GTGCAAGATGATTCAGAGCGGCGAGCGGTGAGAGGCGCTTTGTACCTTGGACATGGAA 1323
QY 421 AspCysGlyTyraAsnIleProGlnThraPgluSerThr 433
DB 1324 GACTGGCTACCACTTCCACAGACAGATGATCAACC 1362

RESULT 3
US-11-090-866-1
Sequence 1, Application US/11090866
Publication No. US20050164294A1
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Basl, Guribai
APPLICANT: Doane, Minh Tam
APPLICANT: Frigon, Normand
APPLICANT: John, Varghese
APPLICANT: Power, Michael
APPLICANT: Sinha, Sukanto
APPLICANT: Tatsuho, Gwen
APPLICANT: Tung, Jay
APPLICANT: Wang, Shuwen
APPLICANT: McConlogue, Lisa
TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
FILE REFERENCE: 228-US-NEW2C12
CURRENT FILING DATE: 2005-03-25
PRIOR FILING DATE: 2000-11-28
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; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-090-866-1

Alignment Scores:
Pred. No.:      8,54e-269      Length:      1503
Score:          2267.00      Matches:      429
Percent Similarity: 99.31%      Conservative: 1
Best Local Similarity: 99.08%      Mismatches: 3
Query Match:      99.08%      Indels:      0
DB:                24      Gaps:        0

US-10-726-967a-84 (1-433) x US-11-090-866-1 (1-1503)

QY 1 ThcGlnHsGlyIleatgLeuProLeuAArgSerGlyLeuGlyValAProLeuGlyLeu 20
Db 64 ACCAGAGCAGGCAATCCGGCTGCCCTCCGACGCGCTGGGGGGGCGCCCTGGGGCTG 123
QY 21 GluIleAenLeuGluThraArgGluGluProGluGluProGlyAraArgGlySerPheVal 40
Db 124 CGGCTGCCCGGAGAGCCGACGAAAGCCGAGAGAGCCGCGCGGAGGGGAGCTTTGTG 183
QY 41 GluMetValAspAenLeuAArgGlyLysSerGlyGlyGlyTyrTyrValGluMetThrVal 60
Db 184 GAATGATGTCACAACTGAGGGGAGAGAGTCCGGGCAAGGCTACTACATGAGATGACCGTG 243
QY 61 GlySerProProGluThraAenIleLeuValAspThrGlySerSerAenPheAlaVal 80
Db 244 GGCAGCGCCCGCAGACGCTCAACATCCGTGTGATACAGGACAGATTAATCTTGCACTG 303
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db 304 GGGCTGCCCCCACCCTTCTCTGCAATCCCTACTACACAGGACAGCTGTCCAGCACATAC 363
QY 101 ArgAspLeuAArgGlyValTyrValProTyrThrGlnGlyLysTrpGlnGlyLeu 120
Db 364 CGGAGCTCCGGAGGGGTGTATATGCTTACACCCAGGGGCAAGTGGAGAGGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAenValThrValArgAlaAenIleAla 140
Db 424 GGCACCGCACTGTAAAGCATCCCAATGCCCCCAAGCTACGTGCTGCCAAGCTTCT 483
QY 141 AlaIleThrGluSerAspLysPhePheIleAenGlySerAenTrpGlnGlyIleLeuGly 160
Db 484 GCCATCACTGAATCAAGCAAGTTCTTCACTCAACGCTCTCAACTGGAGAGGATCCTGGGG 543
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 544 CTGGCTATGCTGAGATTGCCAGGCTGACGACTCCCTGGAGGCTTTCTTTGACATCTCTG 603
QY 181 ValLysGlnThrHisValProAenLeuPheSerLeuGlnLeuGlyValAglYpHePro 200
Db 604 GTAAAGACAGACCAGATGCCAACCTCTTCTCCCTGCGAGCTTTGTGGTGGCTTCCCC 663
QY 201 LeuAenGlnSerGluValLeuAlaSerValAglYpSerMetIleIleGlyGlyIleAsp 220
Db 664 CTCACCAAGCTCTGAAGTCTGCTCTCTCTGAGAGGAGACATGATGAGATGAGATGAC 723
QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleAraArgGluTyrTyrGlu 240
Db 724 CACTCGCTGTACAGAGGAGTCTCTGTGTATACACCCATCCGCGGAGGTGTATTATGAG 783
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QY 241 ValIleIleValAraValGluIleAenGlyGlnAenPheLysMetAspCyLeGluTyr 260
Db 784 GTGATCATTTGGCGGGTGGAGATCAATGGACAGATCTGAATAATGGACTGCAGAGATAC 843
QY 261 AenTyrAspLysSerIleValAspSerGlyThrThrAenLeuAraGluProLysVal 280
Db 844 AACTATGACAAAGAGATGTGGACAGTGGACACCAACTTCTTGTGCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValLysSerIleLysAlaIleSerSerThrGlyLysPheProAspGly 300
Db 904 TTTGAAGCTGACATCAATTCATCAAGGACCTTCTCCAGGAGAAAGTTCCTGATGT 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTyrAenIlePhe 320
Db 964 TTCTGGCTAAGAGAGAGCTGTGTGCTGGCAACAGGACACCCCTTGGACATTTTC 1023
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAenGlnSerPheArgIleThrIle 340
Db 1024 CGAGTCATCTACTCTTACCTTATGAGGTACCAACAGTCCCTTCCGATCACCATC 1083
QY 341 LeuProGlnGlnTyrLeuAraGProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1084 CTTCGGAGAGAAATACCTGCGGCCAGTGGAAAGATGTGCCACGTCCCAAGGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1144 AAGTTGCAATCTCAAGTATCATCCACGGGCACTGTATGGAGACTGTATCATGAGGGG 1203
QY 381 PheTyrValValPheAspAraGluAraGlyLysIleGlyPheAlaValSerIleCysHis 400
Db 1204 TTCTACCTTGTCTTTGATCGGGCCCAAAACGAATTTGGCTTGTCTGACGGCTTGCCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1264 GTGCACATGATGTTACAGAGCGGACGGGTGAAGGCCCTTTGTGTACCTTGGACATGGAA 1323
QY 421 AspCysGlyTyrAenIleProGlnThrAspGluSerThr 433
Db 1324 GACTGTGGCTTAACAATTCACACAGACAGATGATCAACC 1362

RESULT 4
; Sequence 1, Application US/11069377
; Publication No. US20050170489A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Guridbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Simha, Sukanco
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; FILE REFERENCE: 228-US-NEW208
; CURRENT APPLICATION NUMBER: US/11/069,377
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: 60/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
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LENGTH: 1503
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-069-377-1

Alignment Scores:

Score:	8,54e-269	Length:	1503
Percent Similarity:	2267.00	Matches:	429
Best Local Similarity:	99.31*	Conservative:	1
Query Match:	99.08*	Mismatches:	3
		Indels:	0
		Gaps:	0

US-10-726-967a-84 (1-433) x US-11-069-377-1 (1-1503)

```

QY      1 ThrGlnHISGLYIleArgLeuProLeuArgSerGlyLeuGlyGlyAlaProLeuGlyLeu 20
DB      64 ACCGACGCGGATCCGGCTCCCTGCGCAGCGGCTGGGGGCGCCCTGGGGCTG 123
QY      21 GlnIleAsnLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
DB      124 CGGCTGCGCCGGGAGACCGACGAGAGCCCGAGAGCCCGCGCGAGGGGCGAGCTTTGCG 183
QY      41 GlnMetValAspAsnLeuArgGlyLeuSerGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 60
DB      184 GAGATGCTGACCACTGAGGGGCGACGCGGGCGAGGCTACTTACCTGAGATGACCGTG 243
QY      61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
DB      244 GCGAGCCCCCGACAGCGCTCAACATCTCGTGATGATACAGCAGCATTTTGACAGT 303
QY      81 GlyAlaAlaProHISerProPheLeuHISArgTYrTYrGlnArgGlnLeuSerSerThrTYr 100
DB      304 GGGTGGCCCCCAACCCCTTCCGTCGACTACTACCAAGGCGAGCTGTCCAGCATATAC 363
QY      101 ArgAspLeuArgGlyGlyValTYrValProTYrThrGlnGlyGlyGlyGlyGlyGlyGly 120
DB      364 CGGAGCTCCGGAGGGGTGTATGTGCGCTTACACCAAGGCGAGGAGGGGAGGCTG 423
QY      121 GlyThrAspLeuValSerIleProHISGlyProAsnValThrValArgAlaAsnIleAla 140
DB      424 GGCACCGACCTGGTATGCAATCCCGCATGGCCCAAGCTCACTGTGCTGCCAATTTGCT 483
QY      141 AlaIleThrGlySerAspLeuPhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160
DB      484 GCCATCACTGAATCAACAAAGTTCTTCACTCAACAGGCTCCCAAGGAGCATCTGGGG 543
QY      161 LeuAlaTYrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB      544 CTGGCTATGCTGAGATTGCGCAGGCTGACGACTCCCTGAGCCTTCTTTGACTCTCTG 603
QY      181 ValIleGlyThrIleValProAsnLeuPheSerLeuGlnLeuGlyGlyAlaGlyPhePro 200
DB      604 GTAAACAGACCCACGTTCCCAACCTTCTCCCTGAGCTTTGTGTGCTGCTTCCCTCC 663
QY      201 LeuAsnGlnSerGluValIleuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
DB      664 CTCACACAGCTGAGAGTGGCTGCTGTGCGAGGGAGCATGATTCATTGGAGGTATCGAC 723
QY      221 HISerLeuTYrThrGlySerLeuTYrTYrThrProIleArgArgGluTYrTYrGln 240
DB      724 CACTCGCTGTACACAGGAGCTCTCTGTGTATACACCCATCCGGGGAGGTGTATGTAG 783
QY      241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuMetAspCysGlyGluTYr 260
DB      784 GTATCATTTGTGGGGAGATCATGACAGGATTTGAAATTCAGATCTCAGAGAGTAC 843
QY      261 AsnTYrAspLeuSerIleValAspSerGlyThrThrAsnLeuArgLeuProGlyGlyVal 280
DB      844 AACTATGACAAAGGATTTGTGACAGTGGCACCACCAACTTGTGTTGGCCCAAGAAAGTG 903
QY      281 PheGluAlaAlaValIleSerIleGlyAlaIleSerSerThrGluGlyPheProAspGly 300

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DB      904 TTTGAGCTGACGATCAATTCATCAAGGACGCTCTCCACGAGAGAGTTCCGTAGTGT 963
QY      301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrTrpProTrpAsnIlePhe 320
DB      964 TTCTGGCTAGGAGAGACAGCTGTGTGTGCGCAGACGAGCACCCCTTGAAACATTTTC 1023
QY      321 ProValIleSerLeuTYrLeuMetGlyGlyValIleThrAsnGlnSerPheArgIleThrIle 340
DB      1024 CAGTCACTTCACTTACTTAATGGGTGATACCAACAGTCTCTCCGATACCAATC 1083
QY      341 LeuProGlnGlnTYrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTYr 360
DB      1084 CTTCGAGCAATACCTCGCGGACAGTGAAGATGGCCAGTCCCAAGACGACTGTATC 1143
QY      361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGlyGly 380
DB      1144 AAGTTGCACTCTCACAGATTCACCGGCGACTGTATAGGAGCTGTATATCATGAGAGGC 1203
QY      381 PheTYrValIlePheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
DB      1204 TTCTACGTTGCTTTGATCGGCGCCGAAAGAAATGGCTTTGCTGTACGCCCTTGCCAT 1263
QY      401 ValHISAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB      1264 GTGCAGATGATGATTCAAGACGCGCAGCGGTGAGAGCCCTTTGTCACTTGACATGMA 1323
QY      421 AspCysGlyTYrAsnIleProGlnThrAspGluSerThr 433
DB      1324 GACTGTGCTACCAACATTCACAGACAGATGATGATCAAC 1362

RESULT 5
US-11-090-872-1
; Sequence 1, Application US/11090872
; Publication No. US2005017788A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Basl, Gurigbal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tateano, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 228-US-NEW2C11
; CURRENT APPLICATION NUMBER: US/11/090,872
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 09/723,722
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1503
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-090-872-1

Alignment Scores:
Pred. No.: 8,54e-269 Length: 1503
Score: 2267.00 Matches: 429
Percent Similarity: 99.31* Conservative: 1

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Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 24 Gaps: 0
US-10-726-967a-84 (1-433) x US-11-090-872-1 (1-1503)

QY 1 ThGlnHieGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB 64 ACCGACGACGACATCCGGCTGCCCCCTGCGACGCGCTGGGGGAGCGCCCCCTGGGGCTG 123
QY 21 GluIleAsnLeuGlyIleArgLeuGlyLeuProGlyLeuProGlyValArgArgGlySerPheVal 40
DB 124 CGGCTGCCCCGGGAGACCGACGAGAGCCGAGAGGCCGCGCGAGGGGACCTTTGTC 183
QY 41 GluMetValAspAsnLeuArgGlyLeuSerGlyGlyGlyValGlyValGluMetThrVal 60
DB 184 GAGATGTGTGACACCTGAGGGGCAAGTCGGGGCAGGGCTACTACCTGAGATGACCGTG 243
QY 61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
DB 244 GCGAGCCCCCGACGACGCTCAACATCTGTGGATACAGGACGACGATTACTTGCAGTG 303
QY 81 GlyAlaAlaProHisProPheLeuHisArgValArgGlnLeuSerSerThrVal 100
DB 304 GGTGCTGCCCCCACCCTTCTGCACTGCTACTACAGAGGACGCTGCCAGACATAC 363
QY 101 ArgAspLeuArgGlyValValValProValProValThrGlnGlyValGlyTrpGluGlyLeu 120
DB 364 CGGACCTCCGAGAGGGGTGTATGTGCTTACACCCAGGAGGAGTGGAGAGGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
DB 424 GGCACGACCTGGTATGACATCCGCCCATGCCCCAAGTCACTGTGGTCCAACTTGGT 483
QY 141 AlaIleThrGluSerAspLeuPhePheIleAsnGlySerAsnTrpGluGlyIleGly 160
DB 484 GGCATCTACGAAATCACAAGATCTTTCATCAACGCGCTCCACGAGGAGGACCTCGGGG 543
QY 161 LeuAlaValAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB 544 CTGGCTTATGCTGACATTCGACGCTTCCAGACTCCCTGAGACCTTTCTTATACCTCG 603
QY 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
DB 604 GTAAAGCAGACCCAGCTTCCCAACTCTCTCCCTGACGCTTGTGGGCTGGCTCCCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
DB 664 CTCAACCACTGAAAGTGTGGCTCTGTGCGAGGAGATGATATGAGAGTATCGAC 723
QY 221 HisSerLeuValThrGlySerLeuTrpValThrProIleArgAlaGluTrpValGly 240
DB 724 CACTGCTGTACACAGGAGCTCTGTGATACACCCATCCGGGAGGTGATATATAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyIleAspLeuValMetAspCysLeuGlyVal 260
DB 784 GTGATCATTTGCGGGGTGAGATCAATGACAGATCTGAAAATGACCTGCACAGAGATAC 843
QY 261 AsnTrpAspLeuSerIleValAspSerGlyThrThrAsnLeuArgLeuProValGlyVal 280
DB 844 AACTATGACAGACATTTGTGACAGTGCACACCAACCTTCGTTTCCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValLeuSerIleValAlaAspSerThrGluValPheProAspGly 300
DB 904 TTTGAAAGCTGAGATCAATTCATCAAGGACGCTCTCCAGAGAAATTCCTGATGT 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
DB 964 TTTGCGCTAGAGAGACAGCTGGTGTGCTGGCAGAGGACACACCCCTTGGAAATTTTC 1023
QY 321 ProValIleSerLeuValLeuMetGlyValValThrAsnGlnSerPheArgIleThrIle 340
DB 1024 CCAATCATCTACTTAAATGGGTAGGTTACCAACGACGCTTCCTCGCATCAATC 1083

QY 341 LeuProGlnGlyIleArgLeuProValGluIleAspValAlaThrSerGlnAspAspCysVal 360
DB 1084 CTTCGCGACCAATACCTCGGCGCAGTGGAAATGTGGCCACGTCCCAAGACGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
DB 1144 AAGTTTGCATCTCACTACATTCACACGGGCTGTATGGAGCTGTATCATCATGAGGGC 1203
QY 381 PheValValPheAspArgAlaArgGlyValGlyIleGlyPheAlaValSerAlaCysHis 400
DB 1204 TTTCTAGCTGTCTTGTATCGGCGCCGAAACGAATGTGCTGTGACAGGCTTGGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1264 GTGACGATGATTCAGGACGCGAGCGGTGGAAAGCCCTTTTGTCACTTGGACATGGAA 1323
QY 421 AspCysGlyValAsnIleProGlnThrAspGluSerThr 433
DB 1324 GACTGTGCTACAACTTCCACAGACAGATGATCAACC 1362

RESULT 6
US-10-214-932-103
Sequence 103, Application US/10214932
Publication No. US20030100707A1
GENERAL INFORMATION:
APPLICANT: HWANG, Inman
APPLICANT: KIM, Dae Heon
APPLICANT: LEE, Yong Jik
TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
FILE REFERENCE: AP802/US
CURRENT APPLICATION NUMBER: US/10/214,932
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn version 3.1
SEQ ID NO 103
LENGTH: 1506
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: gene
LOCATION: (1)..(1506)
OTHER INFORMATION: Gene for APP beta-secretase
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1503)
OTHER INFORMATION: APP beta-secretase
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank/AF201468
DATABASE ENTRY DATE: 1999-12-19
US-10-214-932-103

Alignment Scores:
Pred. No.: 8,57e-269 Length: 1506
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
Gaps: 0

US-10-726-967a-84 (1-433) x US-10-214-932-103 (1-1506)

QY 1 ThGlnHieGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB 64 ACCGACGACGACATCCGGCTGCCCCCTGCGACGCGCTGGGGGAGCGCCCCCTGGGGCTG 123
QY 21 GluIleAsnLeuGlyIleArgLeuGlyLeuProGlyLeuProGlyValArgArgGlySerPheVal 40
DB 124 CGGCTGCCCCGGGAGACCGACGAGAGCCGAGAGGCCGCGCGAGGGGACCTTTGTC 183
QY 41 GluMetValAspAsnLeuArgGlyLeuSerGlyGlyGlyValGlyValGluMetThrVal 60
DB 184 GAGATGTGTGACACCTGAGGGGCAAGTCGGGGCAGGGCTACTACCTGAGATGACCGTG 243

QY 61 GYserProGln1ThrLeuasn1leuVal1AspThrGlySerSeranphealVal1 80
DB 244 GGCACGCCCCCGACAGCGCTCAACATCTGGTGAATACGAGCAGCATTTGCGAGT 303
QY 81 GYAla1a1aProHiProPheleuHiSaGTYTYYTGlnArgGlnLeuSerThrTYR 100
DB 304 GGTGTGCCCCCGACCCCTTCTGCACTGCTACTACAGAGCAGCTGTCCAGCATAVC 363
QY 101 AGsApLeuArgGlyVal1TYRVal1ProTYRThrGlnGlyLeuSerThrTYR 120
DB 364 CGGAACCTCCGAAAGGGTGTGTGTGTGCTTACACCCAGGCAAGTGGGAAGGAGCTG 423
QY 121 GYThrAspLeuValSer1leProHiGlyProasnVal1ThrValArgAlaasn1leAla 140
DB 424 GGCACGCACTGGTAAAGCATCCCGCCCAAGCTGTCAGTGTGGCTCCAACTTGCT 483
QY 141 Ala1leThrGlySerAspLysPhePhe1leasnGlySerSeranThrGlyLeuGly 160
DB 484 GCCATCACTGAATCAGACAAATTCTTCATCAACGGCTCCAACTGGGAAAGCATCTGGG 543
QY 161 LeuAlaTYRAlaGln1leAlaArgProAspAspSerLeuGlnProPhePheAspSerLeu 180
DB 544 CTGGCTAATGCTGAATGCTGACGGCTTGACGACTCCCTGAGCCTTTCTTGACTCTCG 603
QY 181 Val1lyeGlnThrHiVal1ProasnLeuPheSerLeuGlnLeuGlyVal1aGlyPhePro 200
DB 604 GTPAAGCAACCACTTCACCACTCTTCTGCTGAGCTTGTGTGCTGCTGCTGCTGCTG 663
QY 201 LeuasnGlnSerGlyVal1leuVal1AspSerVal1GlyGlySerMet1le1leGlyVal1leAsp 220
DB 664 CTCACACACTGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 723
QY 221 HisSerLeuTYRThrGlySerLeuTYRThrPro1leArgArgGlyTYRThrGlyVal 240
DB 724 CACTGCTGTACACAGCGAGCTCTCTGTATACCCATCCGCGGAGTGTATATGAG 783
QY 241 Val1le1leVal1ArgVal1Gln1leasnGlyGlnAspLeuLysMetAspCysLysGlyTYR 260
DB 784 GTGATCATTTGTGGGGTGGAGATCAATGACAGATCTGAATATGACTCAAGAGTAC 843
QY 261 AsnTYRAspLysSer1leVal1AspSerGlyTYRThrAsnLeuArgLeuProLysVal 280
DB 844 AACTATGACAAAGCAATGTCAGTGGACACCAACCTTGTGTTGCCAAGAAAGT 903
QY 281 PheGlnAlaAlaVal1LysSer1leLysAlaAlaSerSerThrGlyLysPheProAspGly 300
DB 904 TTTGAAGCTGCACTCAAAATCATCAAGGACGCTCTCCACGAGAAATTCCTGATGCT 963
QY 301 PheTYRLeuGlyGlyGlnLeuVal1CysTYRAla1aGlyTYRThrProTYRAsn1lePhe 320
DB 964 TTTGCTGTAAGAAAGCATGCTGTGTGTGTGCTGCAAGGACGACCACTTGGAACATTTTC 1023
QY 321 ProVal1leSerLeuTYRLeuMetGlyGlyVal1ThrAsnGlnSerPheArg1leThr1le 340
DB 1024 CCACTCATCTCACTCACTCAATAGGTGAGTTACCAACCAAGTCTTCCCATCACCATC 1083
QY 341 LeuProGlnGlnTYRLeuArgProVal1GlnAspVal1AlaThrSerGlnAspAspCysTYR 360
DB 1084 CTTCCGAGCAATACCTGCGGCGAGTGAAGATGTGCCCATGCCCAAGCACTGTAC 1143
QY 361 LysPheAla1leSerGlnSerSerThrGlyTYRVal1MetGlyVal1leMetGlyGly 380
DB 1144 AAGTTTGCCATCTCAAGTATCCACGGGCACTGTTATGGAAGCTGTTATCATGAGGCGC 1203
QY 381 PheTYRVal1Val1PheAspArgAlaArgLysArg1leGlyPheAlaVal1SerAlaCysHis 400
DB 1204 TTTCAAGTGTCTTGTATCGGGCCCGAAACGAATGTGCTTGTGTGCTGCTGCTGCTGCT 1263
QY 401 Val1HisAspGlnPheArgThrAlaAlaVal1GlnGlyProPheVal1ThrLeuAspMetGly 420
DB 1264 GTGACGATGATTCAGAGAGCGGCGGTGGAAGGCCCTTTGTACCTTGACATGAA 1323

QY 421 AspCysGlyTYRAsn1leProGlnThrAspGlnSerThr 433
DB 1324 GACTGTGGCTACCAATTCACAGACAGATGATGATACC 1362

RESULT 7
US-10-281-092-5
Sequence 5, Application US/10281092
Publication No. US20040121947A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Arun K.
APPLICANT: Tang, Jordan J.N.
APPLICANT: Bilcer, Geoffrey
APPLICANT: Chang, Wampin
APPLICANT: Hong, Lin
APPLICANT: Koelsch, Gerald E.
APPLICANT: Loy, Jeffrey A.
APPLICANT: Turner, Robert T., III
APPLICANT: Devasumadrum, Thippeswamy
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT BETA-SECRETASE
TITLE OF INVENTION: ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: 2932.1001-004
CURRENT FILING DATE: 2002-10-23
PRIOR FILING DATE: 2002-10-23
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: PCT US01/50826
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/258, 705
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/275, 756
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 60/335, 952
PRIOR FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/333, 545
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 60/348, 464
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/348, 615
PRIOR FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/390, 804
PRIOR FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: US 60/397, 557
PRIOR FILING DATE: 2002-07-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: memapsin 2
US-10-281-092-5

Alignment Scores:
Pred. No.: 8,576-269 Length: 1506
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 19 Gaps: 0

US-10-726-967a-84 (1-433) x US-10-281-092-5 (1-1506)

QY 1 ThrGlnHisGly1leArgLeuProLeuArgSerGlyLeuGlyVal1aProLeuGlyLeu 20
DB 64 ACCCAAGCAGCGCATCCGCGCTGCCCTGCGCAGCGGCTGGGAGGCGCCCCCTCGGGGCTG 123
QY 21 Gln1leAsnLeuGlnThrAspGlnGlnGlnProGlnGlnProGlnVal1ArgArgGlySerPheVal 40
DB 124 CGGCTGCCCGGAGACCGACGAAAGAGCCGAGAGACCCGCGCGAGGCGGCACTTTGTG 183
QY 41 GlnMetVal1AspAsnLeuArgGlyLysSerGlyGlnGlyTYRThrTYRVal1GlnMetThrVal 60

Db 184 GAGATGGGAGCACTGAGGGGCAAGTCGGGGGAGGGCTACTACGAGGAGTACCGCTG 243
Qy 61 GlycerProProGlnThrLeuAsnIleValAspThrGlySerSerAspPheAlaVal 80
Db 244 GGGAGCCCCCGGAGAGGCTCAACATCTGGTGTAGTACAGGACAGCACTTAATTGGCAGTG 303
Qy 81 G1YAlaIaIaProHISProPheLeuHISArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db 304 GGTCTGCCCCCCCCCTTCTCTGCACTGCTACTACAGAGAGAGCTGTCCAGACACTAC 363
Qy 101 ArgAspLeuArgGlyValIYrValProTyrThrGlnGlyLysTrpGlnGlyValLeu 120
Db 364 CGGAGCTCCGGAGGGGTGTGTATGTGCCCCCTACAGCCAGGGGCAAGTGGAGAGGGAGCTG 423
Qy 121 G1YThrAspLeuValSerIleProHISGlyProAsnValThrValAlaAsnIleAla 140
Db 424 GGCACCGACCTGGTAAGCATCCCCCATGGCCCCCAAGCTGCTGCTGCAACATTTGCT 483
Qy 141 AlaIleThrGlnSerAspLysPhePheIleAsnGlySerAsnTrpGlnGlyIleLeuGly 160
Db 484 GCATCATCTGAATCAGACAGTTCTTCATCAACGGCTCCAACTGGGAGGCACTCTGGGG 543
Qy 161 LeuAlaTyrAlaGlnIleAlaArgProAspAspSerLeuGlnProPheAspSerLeu 180
Db 544 CTGCGCTATCTGAGATTCGACAGGCTGACGACTCCCTGGAGCTTTCTTTGACTCTGTG 603
Qy 181 ValIleGlnThrHISValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
Db 604 GTAAAGCAGACCCAGCTTCCAACTCTCTCCCTGAGCTTGTGTGTGTGTGTGTGTGTG 663
Qy 201 LeuAsnGlnSerGlnValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
Db 664 CTCACACAGCTGTAAGTGTGGCTCTGTGTGAGGGAGATGATTCATTGGAGTATCGAC 723
Qy 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGlnTyrTyrGln 240
Db 724 CACTCGCTGTACACAGGCACTCTGTGTACACCACTCCGGGGAGGTGTATGTATGAG 783
Qy 241 ValIleIleValArgValGlnIleAsnGlyGlnAspLeuIleMetAspCysLysGlnTyr 260
Db 784 GTCATCATTTGTGGGGTGGAGATCAATGACAGAGATCTGAATATGACTGCAAGAGATAC 843
Qy 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 844 AACTATGACAGAGCATTTGTGGACAGTGGCAACCACTTCGTTTGGCCAAAGAAAGTG 903
Qy 281 PheGlnAlaIaValLysSerIleLysAlaIaSerSerThrGlnLysPheProAspGly 300
Db 904 TTTGAAGCTGAGTCAAAATTCATCAAGGCAAGCTCTCTCCAGAGAAATTCCTATGAT 963
Qy 301 PheTrpLeuGlyGlnGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
Db 964 TTCTGGCTAGGAGAGCACTGGTGTGTGTGGCAAGGAGCAACCCCTTGGAAKATTTTC 1023
Qy 321 ProValIleSerLeuTyrIleuMetGlyValValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAAGTCATCTCACTTAACCTAATGGGTGAGTTTACCAACCACTCTCCGCTACCACTC 1083
Qy 341 LeuProGlnGlnTyrIleuArgProValGlnAspValAlaThrSerGlnAspAspCysTyr 360
Db 1084 CTTCGCGACCAATACCTCGGGGCAAGTGGAGATGTGGCCATCCCAAGACACATGTTAC 1143
Qy 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGlnGly 380
Db 1144 AAGTTTGCATCTCAAGTCAACGCGGCACTGTTATGGGAGCTGTTATCATGAGGGGC 1203
Qy 381 PheTyrValIaIaPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1204 TTCACGTTGTCTTGTATGTGGCCCGAAACCAATTTGCTTGTGTGTGTGTGTGTGTGTG 1263
Qy 401 ValHisAspGlnPheArgThrAlaIaValGlnGlyProPheValThrLeuAspMetGln 420

Db 1264 GTCACAGATGAGTTTCAGACGCGACGGGTGAGAGGCCCTTTTGTGACTTGGACATGGA 1323
Qy 421 AspCysGlyTyrAsnIleProGlnThrAspGlnSerThr 433
Db 1324 GACTGTGGCTACAACTTCCACAGACAGATGATGATCAACC 1362
RESULT 8
US-10-275-339A-6
; Sequence 6, Application US/10275339A
; Publication No. US20040110743A1
; GENERAL INFORMATION:
; APPLICANT: MIYAMOTO, Masami
; APPLICANT: MATSUI, Junji
; APPLICANT: FUKUMOTO, Hiroaki
; APPLICANT: TAKUI, Naoki
; TITLE OF INVENTION: Beta Secretase Inhibitors
; FILE REFERENCE: 2729 USOP
; CURRENT APPLICATION NUMBER: US/10/275,339A
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: PCT/JP01/04144
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: JP 2000-152758
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1.2
; SEQ ID NO 6
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-275-339A-6
Alignment Scores:
Pred. No.: 8 75e-269 Length: 1527
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 19 Gaps: 0
US-10-726-967a-84 (1-433) x US-10-275-339A-6 (1-1527)
Qy 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
Db 64 ACCCAGCAGCGCATCCGGCTGCGCTCGCAGCGGCTGGGGGGCGCCCCCTGGGGCTG 123
Qy 21 GlnIleAsnLeuGlnTrrAspGlnGlnProGlnGlnProGlyArgArgGlySerPheVal 40
Db 124 CGGCTGCCCCGGGAGACCGACGAAGAGCCCGAGAGAGCCCGCGGAGGGGCACTTTGTG 183
Qy 41 GlnMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGlnMetThrVal 60
Db 184 GAGATGTTGAGCAACCTGAGGGGCAAGTCCGGGCAAGGCTACTACAGAGAGTGTCCAGATC 243
Qy 61 GlycerProProGlnThrLeuAsnIleValAspThrGlySerSerAspPheAlaVal 80
Db 244 GGCAGCCCCCGGAGAGGCTCAACATCTGTGTGATACAGGACAGCACTTTCAGTG 303
Qy 81 G1YAlaIaIaProHISProPheLeuHISArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db 304 GGTCTGCCCCCCCCCTTCTCTGCACTGCTACTACAGAGAGAGCTGTCCAGACACTAC 363
Qy 101 ArgAspLeuArgGlyValIYrValProTyrThrGlnGlyLysTrpGlnGlyValLeu 120
Db 364 CGGAGCTCCGGAGGGGTGTGTATGTGCCCCCTACAGCCAGGGGCAAGTGGAGAGGGAGCTG 423
Qy 121 G1YThrAspLeuValSerIleProHISGlyProAsnValThrValAlaAsnIleAla 140
Db 424 GGCACCGACCTGGTAAGCATCCCCCATGGCCCCCAAGCTGCTGCTGCAACATTTGCT 483
Qy 141 AlaIleThrGlnSerAspLysPhePheIleAsnGlySerAsnTrpGlnGlyIleLeuGly 160
Db 484 GCATCATCTGAATCAGACAGTTCTTCATCAACGGCTCCAACTGGGAGGCACTCTGGGG 543

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QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheSerLeu 180
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|
Db 544 CTGGCTTATGCTGAGATTGCTGAGCTTCAAGACTCTCTGAGCTTTCTTTATCTCTG 603
QY 181 ValIleValThrHisValProAsnLeuPheSerLeuGluLeuCyGylValIleGlyPhePro 200
|
|
|
Db 604 GTAAGGACAGACCAAGCTTCCCAACTCTCTCTCCCTGACCTTTGAGTCTGCTGCTCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
|
|
|
Db 664 CTCACACAGTCTGAGTGTGGCTCTGTCTGGAGGAGCATATCATTTGAGAGTATGCAC 723
QY 221 HisSerLeuTyrThrGlySerLeuTyrPylTyrProIleArgArgGluTyrPylTyrGlu 240
|
|
|
Db 724 CACTGCTGTATACAGAGCAAGTCTCTGTATACACCATCCGCGGAGGTATATATGAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLeuMetAspCysIleGlyTyr 260
|
|
|
Db 784 GTGATCATTTGTGGGTGAGATCATGAGACAGATCTGAAAATGAGACTGCAAGAGTAC 843
QY 261 AsnTyrAspIleSerIleValAspSerGlyTyrThrAsnLeuArgLeuProIleVal 280
|
|
|
Db 844 AACTATGACAGAGCATTTGGACAGTGGACACCAACCTTCTGTTGCCAAGAAAGTG 903
QY 281 PheGluAlaAlaValIleSerIleValAlaIleSerThrGluIlePheProAspGly 300
|
|
|
Db 904 TTTGAAAGCTGACGTCAATTCATCAAGGACGCTCTTCCACGAGAAAGTCTCTGATG 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
|
|
|
Db 964 TTCTGGCTTGAAGAGAGCTGTGTCTGTGACAGAGGACCACTCCCTTGAAATTTTC 1023
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
|
|
|
Db 1024 CCAATCATCTCACTCAACATGAGGTGAGTTACCAACAGTCTTCCGATCACATTC 1083
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
|
|
|
Db 1084 CTTCCTCCACCAATACCTGCGGCGGAGGAAAGATGTGCCACCTCCCAAGACGACTTTTC 1143
QY 361 IysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyValAlaIleMetGlyIle 380
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|
|
Db 1144 AAGTTTGCATCTCACAGTATCACAGGACACTGTTATGAGACCTTTATCATGAGGGC 1203
QY 381 PheTyrValIlePheAspArgAlaArgIleGlyPheAlaValSerAlaCysHis 400
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|
|
Db 1204 TTCTACGTTCTCTTGAATGGGCGCCAAAACGAATGGCTTGTCTGTACGCGCTTGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
|
|
|
Db 1264 GTCCACGATGAGTTCAAGGACGCGGAGGTGAAAGGCTTTTGTCACTTGGACATGAA 1323
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGlnSerThr 433
|
|
|
Db 1324 GACTGTGGCTCAACAATTCACAGACAGATGATCAACC 1362
RESULT 9
US-10-322-684-1
; Sequence 1, Application US/10322684
; Publication No. US20030125257A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Assay and screening method for identification of inhibitors of de
; FILE REFERENCE: Case 21066
; CURRENT APPLICATION NUMBER: US/10/322,684
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: EP01130282.5
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1542
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-684-1
Alignment Scores:
Pred. No.: 8,886-269 Length: 1542
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 15 Gaps: 0
US-10-726-967a-84 (1-433) x US-10-322-684-1 (1-1542)
QY 1 ThrGlnHisGlyTyrIleArgLeuProLeuArgSerGlyLeuGlyValProLeuGlyLeu 20
|
|
|
Db 79 ACCCGACACGGGATCCGACTGCGACAGCGGAGCGGAGGTGCACCTTGGAGACTG 138
QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyArgArgGlySerPheVal 40
|
|
|
Db 139 CGGCTGCCCGGAGACGACGACAGAGCCGAGAGCCCGCGCGGAGGCGGACTTTGTG 198
QY 41 GluMetValAspAsnLeuArgGlyIleYsSerGlyGlnGlyTyrTyrValGluMetThrVal 60
|
|
|
Db 199 GAGATGGTGAACAACCTGAGGGGCAAGTCGGGGCAGGCTACTAGTGAAGATGACCGTG 258
QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
|
|
|
Db 259 GGCACACCCCGCCACACGCTCAACATCCTGTGATACAGGACGACGATAACTTGCAGTG 318
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
|
|
|
Db 319 GGTGTGCCCCCACCCTTCTCTGATGCTACTACAGAGGACACTGCCAGCATATC 378
QY 101 ArgAspLeuArgIleGlyValTyrValProTyrThrGlnGlyIleTrpGluGlyLeu 120
|
|
|
Db 379 CGGAGCTCCGGAAGGTGTGTATGTGCTTCAACAGGAGCAAGTGGAGGAGGAGCTG 438
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
|
|
|
Db 439 GGCACCGACCTGTGAAGCATGCCCATGCGCCCAAGTCACTGTGTGCGCAACATGCT 498
QY 141 AlaIleThrGluSerAspIlePhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160
|
|
|
Db 499 GCCATCACTGAATCGACAGATTTCTTATCAACGGCTCCAACTGGAGAGGATCTCGGG 558
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheSerLeu 180
|
|
|
Db 559 CTGGCTTATGCTGAGATTCGAGGCTGACGACTCCCTGGAAGCTTTCTTATCATCTCTG 618
QY 181 ValIleValThrHisValProAsnLeuPheSerLeuGluLeuCyGylValIleGlyPhePro 200
|
|
|
Db 619 GTAAGGACAGACCAAGTCCCAACTCTCTCCCTGACAGCTTTGTGTGCTGCTGCC 678
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
|
|
|
Db 679 CTCACACAGTCTGAGTGTGGCTCTGTCTGAGAGGAGCATATCATTTGAGAGTATGCAC 738
QY 221 HisSerLeuTyrThrGlySerLeuTyrPylTyrProIleArgArgGluTyrPylTyrGlu 240
|
|
|
Db 739 CACTGCTTATACAGAGCATCTGTGTATACACCATCCGCGGAGGTATATATGAG 798
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLeuMetAspCysIleGlyTyr 260
|
|
|
Db 799 GTGATCATTTGTGGGTGAGATCATATGACAGATCTGAAAATGAGACTGCAAGAGTAC 858
QY 261 AsnTyrAspIleSerIleValAspSerGlyTyrThrAsnLeuArgLeuProIleVal 280
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|
|
Db 859 AACTATGACAGAGCATTTGGACAGTGGACACCAACCTTCTGTTGCCAAGAAAGTG 918
QY 281 PheGluAlaAlaValIleSerIleValAlaIleSerThrGluIlePheProAspGly 300
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|
|
Db 919 TTTGAAAGCTGACGTCAAAATTCATCAAGGAGCTCTTCCACGGAAGAAAGTTCTCTGATG 978
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QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
Db 979 TTCTGGCTAGAGAGAGCTGGTGTGTGGCAAGAGGACACCCCTTGGAACTTTTC 1038
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1039 CCAATCATCTCACTCTACTTAATGGGTAGGTTACCAACCAAGTCTTCCGATCAACCATC 1098
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1099 CTTCCGAGCAATATACCTCGCGAGTGGAGATGGCGACGTCACCAAGACGACTGTAC 1158
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1159 AAGTTGGCACTCTCACTCACTATCCAGGACCTGTTATGGAGCTGTATCATGAGAGGC 1218
QY 381 PheTyrValIlePheAspArgAlaArgIleGlyPheAlaValSerAlaCysHis 400
Db 1219 TTCTACGTTGCTTGTGATCGGGCCGAAACGAAATGGCTTGTCTGCACGGCTTGCAT 1278
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
Db 1279 GTGCACGATGAGTTCAAGACGCGAGCGTGGAAAGCCCTTTTGTCACTTGGACATGGAA 1338
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGlnSerThr 433
Db 1339 GACTGTGGCTACACATTCACAGACAGATGAGTCAACC 1377

RESULT 10
US-10-652-927-3
Sequence 3, Application US/10652927
Publication No. US2004004340BA1
GENERAL INFORMATION:
APPLICANT: Gurney et al.
TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
FILE REFERENCE: 29915/6280N3
CURRENT APPLICATION NUMBER: US/10/652,927
CURRENT FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: 09/794,925
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2070
TYPE: DNA
ORGANISM: Homo sapiens
US-10-652-927-3

Alignment Scores:
Pred. No.: 1,396-268 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 3
Best Local Similarity: 99.08% Mismatches: 1
Query Match: 99.08% Indels: 0
DB: 18 Gaps: 0

US-10-726-967a-84 (1-433) x US-10-652-927-3 (1-2070)

QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyAlaProLeuGlyLeu 20
Db 64 ACCGACGACGGGATCCGGCTCCCTCGCGAGCGGCTGGGGGGCGCCCCCTTGGGCTG 123

QY 21 GluIleAsnLeuGluThrAspGlnGluProGlnGluIleProGlyValArgArgGlySerPheVal 40
Db 124 CGGCTCCCGGGAGACCAAGACAGCCGAGGAGCCGGCCGAGAGGAGGAGCTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
Db 184 GAGATGTGTGACAACTGAGGGGCAAGTGGGGGAGGGCTACTCTGAGATACACCTG 243
QY 61 GlySerProProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 244 GCGAGCCCCGAGACACCTCAACATCTGTGTGATACAGGACACAGTAATCTTGCAGTG 303
QY 81 GlyAlaAlaProHisAspPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db 304 GGTGTGCCCCCGACCCCTTCTCTCATCGCTACACAGAGGAGCTGTCCAGCACATAC 363
QY 101 ArgAspLeuArgGlyValTyrValProTyrThrGlnGlyTyrTrpGlnGlyLeu 120
Db 364 CGGAGCTCCGGAAGGGGTGTATGTGCCCTACACCCAGGGCAAGTGGAAAGGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 424 GGCACCGACCTGTTAGCATTCGCCATGGCCCAAGCTCATCTGTGCTGCACATTTGCT 483
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTrpGlnGlyIleLeuGly 160
Db 484 GCCATCATCTGATACAGACAAAGTCTTCTCATCAAGGCTCCAACTGGGAAGGCATCTGGG 543
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPheAspSerLeu 180
Db 544 CTGGCTTATGCTGATGATGTGCGAGGCTGACGACATCCCTGTGAGCTTTCTTGTGCTCTG 603
QY 181 ValIysGlnThrHisValProAsnLeuPheSerLeuGlnLeuCysGlyAlaGlyPhePro 200
Db 604 GTAAGGAGACACCACGTTCCCAACTCTTCTCCCTGACACTTGTGTGCTGGCTTCCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyIleAsp 220
Db 664 CTCAACCAAGTCTAAGTGTGGCTCTGTGTGCGAGGAGCATGATCATGAGATATGAC 723
QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
Db 724 CACTCGCTGTACACAGGAGTCTCTGTATACACCATCCGGGAGGTGATATATGAG 783
QY 241 ValIleIleValAlaArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLysGlyTyr 260
Db 784 GTCATCATTTGGGGGTGGAGATCAATGACAGGATCTGAAATGGACTGCMAAGAGTAC 843
QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 844 AACTATGACAAAGCATTTGTGACAGTGGACCAACCACTTCGTTTCCCAAGAAATGTG 903
QY 281 PheGluAlaAlaValIysSerIleLysAlaIleSerSerThrGluLysPheProAspGly 300
Db 904 TTGGAAGTGTGACATAATCCATCAAGGAGGCTCTCCACGAGAAATTTCCATGATGT 963
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
Db 964 TTCTGGCTAGAGAGAGCTGGTGTGTGGCAAGACGACACACCCCTTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1024 CCAATCATCTCACTCTACTTAATGGGTAGGTTACCAACCAAGTCTTCCGATCAACCATC 1083
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1084 CTTCCGAGCAATATACCTCGCGAGTGGAGATGGCGACGTCACCAAGACGACTGTAC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1144 AAGTTGGCACTCTCACTCACTATCCAGGACCTGTTATGGAGCTGTATCATGAGAGGC 1203

QY 381 PheTYValValPheAspArgAlaArglysaRgllleglyPheAlaValSerAlaCyshis 400
DB 1204 TTCTAGTGTCTTGGATCGGGCCGGAACCAATGGCTGTGCTGCGCTTGGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1264 GTGCAGAGATGATGACGAGCGGCGGATGAGAGAGGCCCTTTTGTCACTTGGACATGGAA 1323
QY 421 AspCyGlyTYrAsnIleProGlnThrAspGluSerThr 433
DB 1324 GACTGTGGCTACACATTTCCACGACAGATGATGAACC 1362
RESULT 11
US-10-652-830-3
; Sequence 3, Application US/10652830
; Publication No. US20040048303A1
; GENERAL INFORMATION:
; APPLICANT: Gurney et al.
; TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
; FILE REFERENCE: 29915/6280N1
; CURRENT APPLICATION NUMBER: US/10/652,830
; PRIOR FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: 09/794,925
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2070
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-652-830-3
Alignment Scores:
Pred. No.: 1,396-268 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 18 Indels: 0
Gaps: 0
US-10-726-967a-84 (1-433) x US-10-652-830-3 (1-2070)
QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyGlyAlaProLeuGlyLeu 20
DB 64 ACCACACACGCGCATCCGGCTGCCCTGCCGACGCGCTGGGGGCGCCCTCGGGGCTG 123
QY 21 GluIleAsnLeuGlnThrAspGluGluProGluGluProGlyValArgArgGlySerPheVal 40
DB 124 CGGCTGCCCCGGAGACCGACGAAAGCCCCGAGAGCGCGCGGAGGGGCACTTTGTG 183
QY 41 GluMetValAspAsnLeuArgGlyIleSerGlyGlnGlyTYrTYrValGluMetThrVal 60
DB 184 GAGATGCTGACAACTCGAGGGGCAAGTCGGGGCAAGGCGTACGAGATGACCGTG 243
QY 61 GlySerProGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
DB 244 GGCAGCGCCCGCAGACGCTCAACATCTGTGTGATTCAGGCGACAGTAACTTTGACGTG 303
QY 81 GlyAlaAlaProHisProPheLeuHisArgTYrTYrGlnArgGlnLeuSerSerThrTYr 100
DB 304 GTGTGTGCCCCCACCCTTCTGTGATGGCTACTACGAGGGAGGCTGTCCAGCATATAC 363

QY 101 ArgAspLeuArglyGlyValTYrValProTYrThrGlnGlyIleTYrGluGluLeu 120
DB 384 CGGACCTCCGGAAGGCTGTATGTGCTTACACCCAGGCGCAAGTGGAGAGGAGCTG 423
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
DB 424 GGCACCGACCTGTAAAGCATCCCCCATGGCCCCCAACGTCACGTGCGCGCCAACTTCT 483
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTPGluGlyIleLeuGly 160
DB 484 GCCATCATCTGATCAGACAGAGTTCTTCATCAACGCTCCCACTGGAGAGGCACTCTG363 543
QY 161 LeuAlaTYrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB 544 CTGGCTTAGCTGAGATTGCGAGGCTTACACATCTCCCTGGAGCCTTTTGTGACTCTCTG 603
QY 181 ValIleGlnThrHisValProAsnLeuPheSerLeuGlnLeuCyGlyAlaGlyPhePro 200
DB 604 GPAAAGCAGACCAAGTCCCAACTCTTCTCCCTGACGCTTGTGTGTGCTGTGCTTCCCC 663
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyIleAsp 220
DB 664 CTCAACCAAGTCTGAAGTCTGCTGTGTGAGGAGCATGATCATTTGGAGATTCGAC 723
QY 221 HisSerLeuTYrThrGlySerLeuTPYrThrProIleArgArgGluTPYrTYrGlu 240
DB 724 CACTGCTGTACACAGGCGATCTCTGTGTATACCCATCCGGCGGAGTGGATTTATGAG 783
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCyAlaGlyTYr 260
DB 784 GTCATCATTTGCGGGTGGAGATCAATGACAGATCGAANAATGACTCGCAAGAGTAC 843
QY 261 AsnTYrAspLysSerIleValAspSerGlyTYrThrAsnLeuArgLeuProLysVal 280
DB 844 AACTATGACAGAGCATTTGTGACAGTGGCACCAACCACTTCGTTTGGCCAAAGAAAGT 903
QY 281 PheGluAlaAlaValLysSerIleLysAlaAspSerThrGluLysPheProAspGly 300
DB 904 TTTGAAGCTGACGTAATCAATCAAGGCGCTCTCTCCACGAGAAAGTTCCCTATGT 963
QY 301 PheTYrLeuGlyGluGlnLeuValCySTRGlnAlaGlyTYrThrProTYrAsnIlePhe 320
DB 964 TTCTGGCTRAGAGACACTGTGTGTGTGCGACAGGACCAACCCCTTGGAACTTTTC 1023
QY 321 ProValIleSerLeuTYrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB 1024 CCAGTCATCTCACTCACTAATGGGTGAGTTTACCAACCAAGTCTTCCGCTACACATC 1083
QY 341 LeuProGlnGlnTYrLeuArgProValGluAspValAlaThrSerGlnAspAspCyTYr 360
DB 1084 CTTCGCGCAATATCTGTGCGCAGTGGAGAAATGTGGCCAGTCCCAAGCACTGTATC 1143
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
DB 1144 AGATTGTCATCTTCAAGTCAATCCAGGCGCATCTTTATGGAGCTTTATCATGGAGGCG 1203
QY 381 PheTYrValValPheAspArgAlaArglysaRgllleglyPheAlaValSerAlaCyshis 400
DB 1204 TTCTAGTGTCTTGGATCGGGCCGGAACCAATGGCTGTGCTGCGCTTGGCAT 1263
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1264 GTGCAGAGATGATGACGAGCGGCGGATGAGAGAGGCCCTTTTGTCACTTGGACATGGAA 1323
QY 421 AspCyGlyTYrAsnIleProGlnThrAspGluSerThr 433
DB 1324 GACTGTGGCTACACATTTCCACGACAGATGATGAACC 1362
RESULT 12
US-10-652-045-3
; Sequence 3, Application US/10652045
; Publication No. US20040166507A1
; GENERAL INFORMATION:

APPLICANT: Gurney et al.
TITLE OF INVENTION: Alzheimer's Disease Secretase, APP Substrates Therefor and Uses
FILE REFERENCE: 29915/6280N2
CURRENT APPLICATION NUMBER: US/10/652,045
PRIOR FILING DATE: 2003-08-29
PRIOR APPLICATION NUMBER: 09/794,925
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: 60/101,594
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 3
LENGTH: 2070
TYPE: DNA
ORGANISM: Homo sapiens
US-10-652-045-3

Alignment Scores:
Pred. No.: 1,396-268 Length: 2070
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 19 Gaps: 0

US-10-726-967a-84 (1-433) x US-10-652-045-3 (1-2070)

QY	1	ThGlnHnIsglyIleArgLeuProlLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu	20
DB	64	ACCGAGCAGCGCATCCGGCTGCGCTGCGCAGCGCGCTGGGGGCGCCCTGGGGGCTG	123
QY	21	GluIleAsnLeuGluThrAspGluGluProGluGluProGluValArgArgGlySerPheVal	40
DB	124	CGGCTGCGCGGAGAGCAGCAGAGAGCGCGAGAGCGCGCGAGGGGCGAGCTTTGG	183
QY	41	GluMetValAspAsnLeuArgGlyIleSerGlyGlyGlyValArgValGluMetThrVal	60
DB	184	GAGATGCTGACAACTGAGGGGCAAGTGGGGGAGGCTTACTGATGAGATGACCGTG	243
QY	61	GlySerProGluInThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal	80
DB	244	GGGAGCGCCCGGAGAGCGCTCAACATCTGGTGATACAGGCAAGCATTAATTGGCAGTG	303
QY	81	GlyAlaAlaProIleProPheLeuHnIleArgIleValArgGlnLeuSerSerThrTyr	100
DB	304	GGTGTGCGCCCGCCACCTTCTCTGCTGCTACTACAGAGCAGCTTCCAGCAGCATAC	363
QY	101	ArgAspLeuArgIleGlyValIleValProTyrThrGlnGlyIleValTyrGlyGluLeu	120
DB	364	CGGAGCTCCGAGAGGGTGTATGTATGTCCCTACACCGGCGCAAGTGGAGAGGGAGCTG	423
QY	121	GlyThrAspLeuValSerIleProIleGlyProAsnValThrValArgAlaAsnIleAla	140
DB	424	GGCAGCGAGCTGTAGAGATCCCGCAGCCAGCAGCTGCTGCTGCGCAGCATTTGCT	483
QY	141	AlaIleThrGluSerAspIlePhePheIleAsnGlySerAsnTPGluGlyIleLeuGly	160
DB	484	GGCATCAGTGAATCAGCAAGATTCTTTCATCAACGCTCCCACTGGAGGCACTCTGGGG	543
QY	161	LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu	180
DB	544	CTGGCTTATGCTGATGATGCCAGGCTGACCACTCCCTGGAGCTTCTTTGACTCTCTG	603
QY	181	ValIleGlnIleThrIleValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro	200

DB	604	GTAAGACAGACCGACGTTCCCAACTCTTCTCCGAGCTTTTGGTGTGCTGCTCC	663
QY	201	LeuAsnGlnSerGlyValLeuAlaSerValGlyIleSerMetIleIleGlyIleAsp	220
DB	664	CTAACCAATCTGAAGTCTGCTGCTCTGCTGAGGAGCATGATCATTTGAGGATGAC	723
QY	221	HisSerLeuTyrThrGlySerIleuThrPheProIleArgArgIleTyrTyrGlu	240
DB	724	CAGTGTGTACAGAGAGCTCTGATATACACCATCCGAGGAGTGGATTTATGAG	783
QY	241	ValIleIleValArgValGluIleAsnGlyIleAspLeuIleMetAspCyIleGluTyr	260
DB	784	GTCATCATTTGCTGGGTGAGATCAATGACAGGATCTGAATAATGACTGCAAGAGTAC	843
QY	261	AsnTyrAspIleValAspSerGlyThrThrLeuMetLeuPheProIleValIleVal	280
DB	844	AACTATGACAAAGACATTTGTGACAGTGGACCAACCACTTGTGCTTGGCCCAAGAA	903
QY	281	PheGluAlaAlaValIleSerIleValAlaSerSerThrGluIlePheProAspGly	300
DB	904	TTTGAGCTGCAATCAATCCATCAAGCAGCTCTCCAGAGAAAGTCCCTGATGCT	963
QY	301	PheThrLeuGlyIleGluIleuValCysThrGlnAlaGlyThrThrProTyrPheIlePhe	320
DB	964	TTCTGGCTGAGAGAGCTGTGTGTCTGCAAGAGGCAACCCCTTGAACATTTTC	1023
QY	321	ProValIleSerLeuTyrIleuMetGlyIleValThrAsnGlnSerPheArgIleThrIle	340
DB	1024	CCAGTCACTTCACTTCACTTCAATGAGGAGTTCACCAACAGCTTCTCCGATCACCAC	1083
QY	341	LeuProGlnIleTyrIleuAspProValGluAspValAlaThrSerGlnAspAspCysTyr	360
DB	1084	CTTCGAGGAAATCACTGCGCGCAGTGAAGATGTGCCAGCTCCCAAGACAGCATGTAC	1143
QY	361	IlePheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly	380
DB	1144	AAAGTTGCCATCTCAACATGATCACGGGCACTGTTATGGAGCTGTATCATGAGAGGC	1203
QY	381	PheTyrValAlaPheAspArgAlaArgIleGlyPheAlaValSerAlaCysHis	400
DB	1204	TTCTACGTTGCTTGTATGTGGGCCGAAACGAATGCTTGTGCTGAGCGCTTGCAT	1263
QY	401	ValHisAspGluPheArgThrAlaAlaValGluIleProPheValThrLeuAspMetGlu	420
DB	1264	GTCAGAGATGATTCAGAGCGGAGCGGTGAAGGCCCTTTGTACCTTGAACATGAA	1323
QY	421	AspCysGlyTyrAsnIleProGlnThrAspGluSerThr	433
DB	1324	GACTGTGCTACAACTCCACAGACAGATGATGATCAC	1362

RESULT 13
US-10-940-867-3
Sequence 3, Application US/10940867
Publication No. US20050026256A1
GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Bienkowiak, Michael J.
APPLICANT: Helinikou, Robert L.
APPLICANT: Parodi, Luis A.
APPLICANT: Yan, Riqiang
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Alzheimer's Disease Secretase
FILE REFERENCE: 6177.PCPA
CURRENT APPLICATION NUMBER: US/10/940,867
PRIOR FILING DATE: 2004-09-14
PRIOR APPLICATION NUMBER: US 09/806,194
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/101,594
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 3

Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 24 Gaps: 0
US-10-726-967A-84 (1-433) x US-11-089-918-44 (1-2348)
QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB 369 ACCACGACGAGCATCCGGCTGCCCTCCGACGCGCTGGGGGGCCCCCCCCCGGGGCTG 428
QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGlyValArgArgGlySerPheVal 40
DB 429 CGCGTCCCGCGGAGCCGACGAAAGCCCGAGAGCCCGCGCGGCGGCGGCGCTTTGTTG 488
QY 41 GluMetValAspAsnLeuArgGlyLeuSerGlyGluGlyTyrTyrTyrValGluMetThrVal 60
DB 489 GACATGTGACCACTCGAGGGGAGAGTGGGGCAGGGGCTACTACCTGAGAGTACCGTG 548
QY 61 GlySerProGluGlnThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
DB 549 GGCAGCCCCCGGACGCTCAACATCTGTGTGATACAGGACGACGTAACCTTTCAGTG 608
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerThrTyr 100
DB 609 GGTGCTGCCCCCACCCTTCTCGCATCTACTACAGAGGCGAGCTGTCCAGCACATAC 668
QY 101 ArgAspLeuArgGlyValTyrValProTyrThrGlnGlyLeuThrGluGluGluLeu 120
DB 669 CGGACCTCCGAAAGGTGTGTATGTGCTTACCCCTACACCGGAGAGTGGAGGGAGCTG 728
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
DB 729 GGCACCGACCTGGTATGATCCGCCATGGCCCCCAAGTCACTGTGCTGCCAATTCGT 788
QY 141 AlaIleThrGluSerAspIlePhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160
DB 789 GCATCTACGAAATCAACAAGTCTTCTCATCAACGGCTCCAACTGGAGAGGACCTCTGGGG 848
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
DB 849 CTGGCTTATGCTGAGATTCAGGCTTCAGGCTTCCTGAGACCTTTCTTTTACCTCTG 908
QY 181 ValIlyGlnThrHisValProAsnLeuPheSerLeuGlnLeuGlyValAlaGlyPhePro 200
DB 909 GTAAGACAGACCACTTCCCAACCTCTCTCCCTGACGCTTTGTGGTCTGCTCCGCC 968
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyGlyIleAsp 220
DB 969 CTCAACCAAGTGAAGTGTGCTCTCTCGGAGGAGCATGATCATTTGAGAGTATCGAC 1028
QY 221 HisSerLeuTyrThrGlySerLeuTrpTyrThrProIleArgArgGluTrpTyrGlu 240
DB 1029 CACTGGCTGTACACAGGCACTCTCTGTATACCCATCCGGCGGAGTGGATTTATGAG 1088
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysIlyGluTyr 260
DB 1089 GTGATCATTTGTCGGGTGAGATCAATGAGACAGATCTGAAAAATGAGACTGCAAGAGTAC 1148
QY 261 AsnTyrAspIlySerIleIleValAspSerGlyThrThrAsnLeuArgLeuProIlyVal 280
DB 1149 AACATGACAAAGCATTTGTGAGCAGTGCACCAACCACTTCTGTTCCCAAGAAAGTG 1208
QY 281 PheGluAlaAlaValIlySerIleIleValAspSerThrGluLysPheProAspGly 300
DB 1209 TTTGAAGCTGCAATCCATCAAGGCAAGCTCTCTCCAGGAGAAAGTTCCTGATGAT 1268
QY 301 PheTyrPleuGlyGluGlnLeuValCysTrpGlnAlaGlyTyrThrProTyrAsnIlePhe 320
DB 1269 TTCTGGCTAGAGACAGCTGTGTGTGGCAAGGACCAACCCCTTGGAAACATTTTC 1328
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
DB 1329 CCAATCTCTACTCTAAATGGGTAGATTACCAACAGTCTTCCGATCACCATC 1388

QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
DB 1389 CTTCCGCAATATCTCGGCTCCAGTGTGAAATGTGGCCAGCTCCCAAGACCTGTTAC 1448
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
DB 1449 AAGTTTGCATCTCAAGTATCCACGGGCACTTTATGGAGCTGTATATATGAGAGGC 1508
QY 381 PheTyrValIlePheAspArgAlaArgIleArgIleGlyPheAlaValIleSerAlaCysHis 400
DB 1509 TTCTACGTTGTCTTGTGATCGGGCCGAAACGAATTGGCTTGTCTGCACGCGCTTGCAT 1568
QY 401 ValHisAspGluPheArgThrAlaAlaValGluGlyProPheValThrLeuAspMetGlu 420
DB 1569 GTGACGATGATTCAGGACGGCGGTGGAGGCCCTTTGTACCTTGGACATGGA 1628
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
DB 1629 GACTGTGCTCAACATTTCCACAGACAGATGATCAAC 1667
RESULT 15
US-11-090-866-44
; Sequence 44, Application US/11090866
; Publication No. US20050164294A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Bael, Gurqibal
; APPLICANT: Doane, Minh Tam
; APPLICANT: Frigon, Normand
; APPLICANT: John, Varghese
; APPLICANT: Power, Michael
; APPLICANT: Sinha, Sukanto
; APPLICANT: Tatsuno, Gwen
; APPLICANT: Tung, Jay
; APPLICANT: Wang, Shuwen
; APPLICANT: McConlogue, Lisa
; TITLE OF INVENTION: Beta-Secretase Enzyme Compositions and
; TITLE OF INVENTION: Methode
; FILE REFERENCE: 228-US-NEW2C12
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US/11/090,866
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/501,708
; PRIOR FILING DATE: 2000-02-10
; PRIOR APPLICATION NUMBER: US 09/471,669
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: 60/119,571
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/139,172
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 2348
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-090-866-44
Alignment Scores:
Pred. No.: 1,69e-268 Length: 2348
Score: 2267.00 Matches: 429
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 99.08% Mismatches: 3
Query Match: 99.08% Indels: 0
DB: 24 Gaps: 0
US-10-726-967A-84 (1-433) x US-11-090-866-44 (1-2348)
QY 1 ThrGlnHisGlyIleArgLeuProLeuArgSerGlyLeuGlyValAlaProLeuGlyLeu 20
DB 369 ACCACGACGAGCATCCGGCTGCCCTCCGACGCGCTGGGGGGCCCCCCCCCGGGGCTG 428

QY 21 GluIleAsnLeuGluThrAspGluGluProGluGluProGluValArgArgGlySerPheVal 40
Db 429 CGGCTGCCCCGGAGAGCCGACGAGAGCCGAGAGCCGCGAGGGGACGCTTTGGG 488
QY 41 GluMetValAspAsnLeuArgGlyLysSerGlyGlnGlyTyrTyrValGluMetThrVal 60
Db 489 GAGAGGTGTGACAACTGAGGGGCAAGTGGGGGAGGCTACTAGCTGAGATGACCGG 548
QY 61 GlySerProProGluThrLeuAsnIleLeuValAspThrGlySerSerAsnPheAlaVal 80
Db 549 GGCAGCCCCCGACAGCGCTCAACATCTGTGTGATACAGCAGCAGTAACTTTGACAG 608
QY 81 GlyAlaAlaProHisProPheLeuHisArgTyrTyrGlnArgGlnLeuSerSerThrTyr 100
Db 609 GGTGTGCTGCCCCACCCCTTCTGTCATGCTACTACAGGACAGCTGTCCAGCACATAC 668
QY 101 ArgAspLeuArgLysGlyValTyrValProTyrThrGlnGlyLysTrpGluGluLeu 120
Db 669 CGGGAAGCTCCGGAAGGGGTGTATGTGCTTACACCCAGGCAAGTGGAGAGGGAGCTG 728
QY 121 GlyThrAspLeuValSerIleProHisGlyProAsnValThrValArgAlaAsnIleAla 140
Db 729 GGCACGAGCTGTGTATGACATCCGCCACCGCCCAAGCTCATGTGTGCTGCCAATGCT 788
QY 141 AlaIleThrGluSerAspLysPhePheIleAsnGlySerAsnTrpGluGlyIleLeuGly 160
Db 789 GGCATCATCGAATCAGACAAAGTTCTTCATCAACGGCTCCAACTGGGAGGCAATCTGGGG 848
QY 161 LeuAlaTyrAlaGluIleAlaArgProAspAspSerLeuGluProPhePheAspSerLeu 180
Db 849 CTGGCTATGTGAGATTCGACGCTGAGGCTGACCTCCCTGAGGCTTCTTGTGACTCTCG 908
QY 181 ValLysGluThrHisValProAsnLeuPheSerLeuGlnLeuGlyAlaGlyPhePro 200
Db 909 GTAAAGCAACCAACGCTCCCAACCTTCTCTCCCTGACGCTTGTGTGTGCTTCCCTCC 968
QY 201 LeuAsnGlnSerGluValLeuAlaSerValGlyGlySerMetIleIleGlyIleAsp 220
Db 969 CTCACCACTGTGAGAGTGTGGCTGTGTGCGAGGAGCATGATCATTTGGAGGTATCGAC 1028
QY 221 HisSerLeuTyrThrGlySerLeuTyrTyrThrProIleArgArgGluTyrTyrGlu 240
Db 1029 CACTCGCTGTACACAGGCAAGTCTCTGTGTATACACCATCCGGGGGAGTGTATTATGAG 1088
QY 241 ValIleIleValArgValGluIleAsnGlyGlnAspLeuLysMetAspCysLysGluTyr 260
Db 1089 GTGATCATGTGTGGGTGTGAGATCAATGACAGGATCTGAAATGGAATGCAAGAGTAC 1148
QY 261 AsnTyrAspLysSerIleValAspSerGlyThrThrAsnLeuArgLeuProLysVal 280
Db 1149 AACTATGACAAAGCATTTGTGGACAGTGGCAACCACTTCTTGGCCAAAGAAAGTG 1208
QY 281 PheGluAlaAlaValLysSerIleValAlaSerSerThrGluLysPheProAspGly 300
Db 1209 TTTGAAGCTGCAAGTCAATCCATCAAGGCAAGCTCTCCACGAGAAAGTTCCTGATGGT 1268
QY 301 PheTrpLeuGlyGluGlnLeuValCysTrpGlnAlaGlyThrThrProTrpAsnIlePhe 320
Db 1269 TTTGTGCTAGAGAGAGAGCTGTGTGTGTGCGAAGAGGCAACCCCTTGGAACTTTTC 1328
QY 321 ProValIleSerLeuTyrLeuMetGlyGluValThrAsnGlnSerPheArgIleThrIle 340
Db 1329 CCAGTATCTCATCTTATCTTAATGGGTGAGGTTACCAACCAAGTCTTCCGATCACATC 1388
QY 341 LeuProGlnGlnTyrLeuArgProValGluAspValAlaThrSerGlnAspAspCysTyr 360
Db 1389 CTTCGCGAGCAATACCTGCGGCAAGTGGAGATGTGCCCAAGCAAGCATGTGTAC 1448
QY 361 LysPheAlaIleSerGlnSerSerThrGlyThrValMetGlyAlaValIleMetGluGly 380
Db 1449 AAGTTTGCATCTCAAGTATCAAGGCACTGTTATGGAGCTGTTATCATGAGAGGC 1508

QY 381 PheTyrValValPheAspArgAlaArgLysArgIleGlyPheAlaValSerAlaCysHis 400
Db 1509 TTCTACGTTGCTTGTGATCGGGCCGAAACCAATTGGCTTTGCTGTACGCCCTTGCCAT 1568
QY 401 ValHisAspGluPheArgThrAlaAlaGluGlyProPheValThrLeuAspMetGlu 420
Db 1569 GTGCACATGATGATTCAGACCGGCAAGCGGTGGAAAGGCCCTTTGTCACTTGGACATGGAA 1628
QY 421 AspCysGlyTyrAsnIleProGlnThrAspGluSerThr 433
Db 1629 GACTGTGCTACCAATTCACAGACAGATGATCAACC 1667

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